

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:23:01 ; Search time 16.31 Seconds  
(without alignments)  
871.933 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 760

Sequence: 1 MEPSADWMLTAAARGVREEV.....TRGSNHARIDAAEGSPDIPD 148

Scoring table:

BIOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 283138 seqs, 96089334 residues

T number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	99.1	156	2 JE0141	cyclin dependent k
2	529	69.6	130	2 178845	p15INK4b - mouse
3	522	68.7	138	2 B55479	CDK4 inhibitor p14
4	461.5	60.7	167	2 158352	p16INK4a - mouse
5	258	33.9	164	2 A57378	cyclin-dependent k
6	249	32.8	166	2 A57379	CDK4/CDK6 inhibito
7	244	32.1	166	2 B57378	cyclin-dependent k
8	231.5	30.5	168	2 B57379	CDK4/CDK6 inhibito
9	228.5	30.1	168	2 A55479	CDK6 inhibitor p18
10	209	27.5	41	2 152720	gene p15INK4b prot
11	158	20.8	3924	2 S37431	ankyrin 2, neutroa
12	137.5	18.1	1848	2 S37771	ankyrin, erythrocy
13	137.5	18.1	1862	2 149502	ankyrin - mouse
14	133.5	17.6	1856	2 B35049	ankyrin 1, erythro
15	133.5	17.6	1880	2 A35049	ankyrin 1, erythro
16	133.5	17.6	1881	1 S3HUK	ankyrin 1, erythro
17	131	17.2	857	2 S62684	potassium channel
18	130.5	17.2	1423	2 137275	death-associated p
19	130	17.1	838	2 S33606	potassium channel
20	130	17.1	1765	2 T42714	ankyrin 3, splice
21	130	17.1	1940	2 T42715	ankyrin 3, splice
22	130	17.1	1943	2 T42713	ankyrin 3, splice
23	130	17.1	1961	2 T42716	ankyrin 3, splice
24	128	16.8	4377	2 A55575	ankyrin 3, long sp
25	127.5	16.8	1786	2 A57282	ankyrin-related pr
26	127.5	16.8	1815	2 T15346	elegans ankyrin-re
27	127.5	16.8	1867	2 T15344	ankyrin-related un
28	127.5	16.8	2039	2 T15347	ankyrin-related un
29	126	16.6	247	2 DB4448	probable ankyrin l

30	125	16.4	1964	2 T09059	notch4 - mouse
31	124.5	16.4	209	2 T15888	hypothetical prote
32	121	15.9	237	2 T50984	related to 265 pro
33	121	15.9	888	2 DB4650	probable potassium
34	120	15.8	476	2 T23213	hypothetical prote
35	118.5	15.6	347	2 C40858	GA-binding protein
36	118.5	15.6	382	2 B40858	GA-binding protein
37	117.5	15.5	347	2 C48146	nuclear respirator
38	117.5	15.5	348	2 C38744	nuclear respirator
39	117.5	15.5	360	2 C38743	nuclear respirator
40	117.5	15.5	395	2 C38741	nuclear respirator
41	117	15.4	1435	2 T32930	hypothetical prote
42	116	15.3	1549	2 T13940	ankyrin - fruit fl
43	115.5	15.2	1058	2 DB2654	ankyrin-like prote
44	114	15.0	828	2 T52046	potassium channel
45	114	15.0	2437	2 S42612	transmembrane prot

#### ALIGNMENTS

RESULT 1  
JE0141  
cyclin dependent kinase inhibitor - human  
N:Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor  
C:Species: Homo sapiens (man)  
C>Date: 02-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 19-May-2000  
C:Accession: JE0141; 159268; S39359; 159585; J05679  
R:Huang, C.G.; Deng, W.; Fu, J.L.  
Chin, J. Biotechnol 13, 105-107, 1997  
A:Title: Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.  
A:Reference number: JE0141  
A:Accession: JE0141  
A:Molecule type: mRNA  
A:Residues: 1-156 <HUA>  
A:Experimental source: Hella cell  
R:Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagihara, K.; Hussain, S.P.; Bennett, Proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994  
A:Title: Mutations and altered expression of p16INK4 in human cancer.  
A:Reference number: 159268; MUID:95062202  
A:Accession: 159268  
A:Molecule type: DNA  
A:Status: translation not shown; translated from GB/EHML/DBDJ  
A:Residues: 1-152 <OKA>  
A:Cross-references: GB:L27211; NID:9558656; PIDN:AAA92554.1; PID:9558657  
R:Serrano, M.; Hannon, G.J.; Beach, D.  
Nature 366, 704-707, 1993  
A:Title: A new regulatory motif in cell-cycle control causing specific inhibition of  
A:Reference number: S39359; MUID:94081956  
A:Accession: S39359  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 9-34, 'V', 36-156 <SER>  
A:Note: This sequence is corrected in reference 159268  
R:Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harsman, K.; Tavtigian, S.V.; Science 266, 436-440, 1994  
A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.  
A:Reference number: 159585; MUID:94204645  
A:Accession: 159585  
A:Status: translation not shown; translated from GB/EHML/DBDJ  
A:Molecule type: DNA  
A:Residues: 51-152 <KAM>  
A:Cross-references: GB:S69804; NID:9546272; PIDN:AAD14048.1; PID:94261748  
C:Comment: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 k1  
C:Genetics:  
A:Gene: GDB:CDKN2A; CDK4I; MCM; P16; INK4; MTS1; CMM2; CDKN2  
A:Cross-references: GDB:335362; OMIM:600160  
A:Map position: 9p21-9p21  
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol  
C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 99.1%; Score 753; DB 2; Length 156;  
 Best Local Similarity 99.3%; Pred. No. 1.3e-64;  
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MEPSADMTATAAGRVEEVALLLEAVLPPAPNSYGRPRPIQVMMGSAVAELLILHGA 60  
 |||||  
 Db 9 MEPSADMTATAAGRVEEVALLLEAGALPPAPNSYGRPRPIQVMMGSAVAELLILHGA 68  
 |||||

OY 61 EPNCDPATLTPVPHDAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 120  
 |||||  
 Db 69 EPNCDPATLTPVPHDAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 128  
 |||||

OY 121 YLRAAAGTSGSNHARIDAEPSDIPD 148  
 |||||  
 Db 129 YLRAAAGTSGSNHARIDAEPSDIPD 156  
 |||||

RESULT 2  
 17845  
 p15INK4b - mouse  
 Species: Mus sp. (mouse)  
 Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 19-May-2000  
 C:Accession: I78845

R:Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.; W  
 Oncogene 11, 635-645, 1995  
 A:Title: Cloning and characterization of murine p15INK4a and p15INK4b genes.  
 A:Reference number: 158352; MUID:95380169  
 A:Accession: I78845  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-130 <RES>  
 A:Cross-references: GB:S79252; NID:q1087092; PID:q1087093  
 C:Gene: p15INK4b  
 C:Genetics:  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

Query Match 69.6%; Score 529; DB 2; Length 130;  
 Best Local Similarity 88.3%; Pred. No. 2.4e-43;  
 Matches 106; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 8 LATAAARGVEEYRALLLEAVLPPAPNSYGRPRPIQVMMGSAVAELLILHGAEPNCADP 67  
 |||||  
 Db 10 LATAAARGVEEYRALLLEAGADPNALNRRGRPIQVMMGSAVAELLILHGAEPNCADP 69  
 |||||

OY 68 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 127  
 |||||  
 Db 70 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 129  
 |||||

RESULT 3  
 B55479  
 CDK4 inhibitor p14(INK4B/MTS2) - human  
 N:Alternate names: CDK6-associated protein p15(INK4b); cyclin-dependent kinase inhibitor  
 C:Species: Homo sapiens (man)  
 C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 21-Jul-2000  
 C:Accession: B55479; S47593; I81183; I52713  
 R:Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.;  
 Genes Dev. 8, 2939-2952, 1994  
 A:Title: Growth suppression by p18, a p16(INK4/MTS1) - and p14(INK4B/MTS2) -related CDK6 i  
 A:Reference number: A55479; MUID:95095079  
 A:Accession: B55479  
 A:Molecule type: mRNA  
 A:Residues: 1-138 <GUA>  
 A:Cross-references: GB:U17075; NID:9639715; PID:NAA50075.1; PID:9639716  
 A:Experimental source: HeLa cells  
 R:Hannon, G.J.; Beach, D.  
 Nature 371, 257-261, 1994  
 A:Title: p15(INK4B) is a potential effector of TGF-beta-induced cell cycle arrest.  
 A:Reference number: S47593; MUID:94359613  
 A:Accession: S47593  
 A:Molecule type: mRNA  
 A:Residues: 1-119, 'TP', 22, 24-31, 'HSW', 35-138 <HAN>

A:Cross-references: GB:I36844; NID:9556197; PID:NAA50282.1; PID:9556198  
 A:Experimental source: Hacat cells  
 R:Kam, A.; Grus, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Hatsman, K.; Tavtighian, S.V.;  
 Science 264, 436-440, 1994  
 A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.  
 A:Reference number: I59585; MUID:94204645  
 A:Accession: I81183  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 53-138 <KAN>  
 A:Cross-references: GB:S69805; NID:9546273; PID:AAU14049.1; PID:94261749  
 R:Gen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.; Papadopoulos, N.; Markowitz, S.;  
 Cancer Res. 54, 6353-6358, 1994  
 A:Title: Deletion of p16 and p15 genes in brain tumors.  
 A:Reference number: I52713; MUID:95079408  
 A:Accession: I52713  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-52 <RES>  
 A:Cross-references: GB:S75756; NID:9861470; PID:AAU14186.1; PID:94261886  
 C:Genetics:  
 A:Gene: GDB:CDKN2B; MTS2  
 A:Cross-references: GDB:S79577; OMIM:600431  
 A:Map position: 9p21-9p21  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol  
 C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 68.7%; Score 522; DB 2; Length 138;  
 Best Local Similarity 85.5%; Pred. No. 1.2e-42;  
 Matches 106; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

OY 4 SADWLATAAARGVEEYRALLLEAVLPPAPNSYGRPRPIQVMMGSAVAELLILHGAEPN 63  
 |||||  
 Db 14 SDESLAATAAARGVEYKQRLLEAGADPNNGVRRGRPIQVMMGSAVAELLILHGAEPN 73  
 |||||

OY 64 CADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 123  
 |||||  
 Db 74 CADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAEELGHRDVAR 133  
 |||||

OY 124 AAAG 127  
 |||||  
 Db 134 TATG 137  
 |||||

RESULT 4  
 I58352  
 p16INK4a - mouse  
 Species: Mus sp. (mouse)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 24-Nov-1999  
 C:Accession: I58352  
 R:Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.;  
 Oncogene 11, 635-645, 1995  
 A:Title: Cloning and characterization of murine p16INK4a and p15INK4b genes.  
 A:Reference number: I58352; MUID:95380169  
 A:Accession: I58352  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-167 <RES>  
 A:Cross-references: GB:S79251; NID:q1087090; PID:q1087091  
 C:Genetics:  
 C:Gene: p16INK4a  
 C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol

Query Match 60.7%; Score 461.5; DB 2; Length 167;  
 Best Local Similarity 63.2%; Pred. No. 8.5e-37;  
 Matches 98; Conservative 16; Mismatches 32; Indels 9; Gaps 3;

OY 1 MEPSADMTATAAGRVEEVALLLEAVLPPAPNSYGRPRPIQVMMGSAVAELLILHGA 60  
 |||||  
 Db 1 MEPSADMTATAAGRVEEVALLLEAGVSPAPNSYGRPRPIQVMMGSAVAELLILHGA 59  
 |||||



```
Db      63 PNLRD-GTGFVAVIHDAARAGFLDTYQALLERQAADVNIEDNEGNPLHLAKKEGRLPYVEE   121
Oy      122 LRAAAGTRGSNHRIDAA    140
       | : : |
Db      122 LMKHTACNVGHNNHKGDTA    140

RESULT          9
AS5479
CDK6 inhibitor p18 - human
N:Alternate names: cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent kinase
C:Species: Homo sapiens (man)
C>Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 20-Sep-1999
C:Accession: A55479
R:Guo, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.;
Genes Dev. 8, 2933-2952, 1994
A>Title: Growth suppression by p18, a p16(INK4/MTS1)- and p14(INK4B/MIS2)-related CDK6 i
A:Reference number: A5479; MUID:95095079
A:Accession: A55479
Molecule type: mRNA
Cross-references: GB:D1U704; NID:g639713; PID:NACC50074.1; PID:g639714
CGenetics:
A:Gene: GDB:CDKN2C
A:Cross-references: GDB:594931
A:Map position: lp32-lp32
C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology
C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match           30.1%; Score 228.5; DB 2; Length 168;
Best Local Similarity 40.3%; Pred.No.1.le-14;
Matches 56; Conservative 22; Mismatches 60; Indels 1; Gaps 1;

Oy      2 EPSADMLATAARGVEEVRRALLEVAALPNAPNSYGRRPIQMMSGARVALLELHGAE    61
     |||::|||::|:::|||::||::|||::||::|||::||::|||::|||::|||::|||
Db      3 EPWGEELASAARGDELTSLQNWNVNNAONGFRGLVMKLNGEIARRLLRGAN    62
Oy      62 PNCADPATLTRPVHDAREFGLDTLVYLHRCAGARDVDANGRI.PVLDAELGRDVARY    121
     ::||::|||||||::::|||::|::|::|||::|||::|||::|||::|||::|||::
Db      63 PLCKD-RGGFAVIHHMAARAEGFLTDLTLFEQADVNIEDNEGNLPHLAAREGHLRVVF    121

Oy      122 LRAAAGTRGSNHRIDAA    140
       | : : |
Db      122 LVKHATSNVGHNKKGDTA    140

RESULT         10
#20
A:Gene: p15INK4B protein - rat (fragment)
C:Species: Rattus sp. (rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-May-2000
C:Accession: I52720
R:Knapek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.
C:Accession: I52720
A>Title: Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in kidney epithel]
A:Reference number: I52720; MUID:95228036
A:Accession: I52720
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Repeats: 1-41 <RES>
A:Cross-references: GB:S77734; NID:g998711
C:Genetics:
A:Gene: p15INK4B
C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology
```

Db 1 MMMSGACVAFELLHGAEPPNCADPATLTRPHYDABAREGFLD 41

RESULT 11

S37431 ankynin 2, neuronal long splice form - human

N:Alternate names: ankynin B, 440K splice form; ankynin-B, brain ankynin; non-erythro

N:Contains: ankynin 2, short form

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 13-Aug-1999

C:Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569

R:Chan, W.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37431

A:Accession: S37431

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-3924 <CHA>

A:Cross-references: EMBL:Z26634; NID:g406287; PTDN:CAA81387.1; PID:g406288

R:Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.

J. Cell Biol. 114, 241-253, 1991

A>Title: Isolation and characterization of cDNAs encoding human ankynins reveal

A:Reference number: A39643; MUID:91302466

A:Accession: A39643

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1443,3585-3924 <OTT>

A:Cross-references: EMBL:X56958

R:Se, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Wa

Genomics 10, 858-866, 1991

A>Title: Isolation and chromosomal localization of a novel nonerythroid ankynin gene.

A:Reference number: A40334; MUID:92009921

A:Accession: A40334

A:Molecule type: DNA

A:Residues: 463-474, 'PE', 477-495 <TSE>

A:Cross-references: GB:M37123; NID:g178647; PTDN:AAA62828.1; PID:g178648

R:Chan, W.; Kordell, E.; Bennett, V.

J. Cell Biol. 123, 1463-1473, 1993

A>Title: 440-kD ankyninB: structure of the major developmentally regulated domain and

A:Reference number: A49462; MUID:94075409

A:Accession: A49462

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-3924 <RES>

A:Cross-references: EMBL:Z26634; NID:g406287; PTDN:CAA81387.1; PID:g406288

C:Genetics:

A:Gene: GDB:ANK2

A:Cross-references: GDB:127607; OMIM:106410

A:Map position: 4q25-4q27

C:Superfamily: ankynin, ankynin repeat homology

C:Keywords: alternative splicing

F:2-3924/Product: ankynin 2, long form #status predicted <MAT>

F:2-1443,3585-3924/Product: ankynin 2, short form #status predicted <MA2>

F:63-95/Domain: ankynin repeat homology <AN01>

F:96-128/Domain: ankynin repeat homology <AN02>

F:129-161/Domain: ankynin repeat homology <AN03>

F:162-190/Domain: ankynin repeat homology <AN04>

F:191-223/Domain: ankynin repeat homology <AN05>

F:232-264/Domain: ankynin repeat homology <AN06>

F:265-297/Domain: ankynin repeat homology <AN07>

F:298-330/Domain: ankynin repeat homology <AN08>

F:331-363/Domain: ankynin repeat homology <AN09>

F:364-396/Domain: ankynin repeat homology <AN10>

F:397-429/Domain: ankynin repeat homology <AN11>

F:430-462/Domain: ankynin repeat homology <AN12>

F:463-495/Domain: ankynin repeat homology <AN13>

F:496-528/Domain: ankynin repeat homology <AN14>

F:529-561/Domain: ankynin repeat homology <AN15>





## RESULT 14

B35049

ankyrin 1, erythrocyte splice form 3 - human

N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N:Contains: ankyrin 2.2, erythrocyte

C:Species: Homo sapiens (man)

C:Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 10-Jul-1998

C:Accession: B35049

R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A:Title: cDNA sequence for human erythrocyte ankyrin.

A:Reference number: A35049; M0ID:90175370

A:Accession: B35049

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1856 &lt;LAN&gt;

C:Genetics:

A:Gene: GDB:ANK1; ANK

A:Cross-references: GDB:118737; OMIM:182900

Map position: Bp11.2-Bp11.2

Superfamily: ankyrin; ankyrin repeat homology

Keywords: alternative splicing

F:2-1886/Product: ankyrin 1, erythrocyte form 3 #status predicted &lt;MA1&gt;

F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted &lt;MA2&gt;

F:44-76/Domain: ankyrin repeat homology &lt;AN01&gt;

F:77-109/Domain: ankyrin repeat homology &lt;AN02&gt;

F:110-142/Domain: ankyrin repeat homology &lt;AN03&gt;

F:143-171/Domain: ankyrin repeat homology &lt;AN04&gt;

F:172-204/Domain: ankyrin repeat homology &lt;AN05&gt;

F:205-237/Domain: ankyrin repeat homology &lt;AN06&gt;

F:238-270/Domain: ankyrin repeat homology &lt;AN07&gt;

F:271-303/Domain: ankyrin repeat homology &lt;AN08&gt;

F:304-336/Domain: ankyrin repeat homology &lt;AN09&gt;

F:337-369/Domain: ankyrin repeat homology &lt;AN10&gt;

F:370-402/Domain: ankyrin repeat homology &lt;AN11&gt;

F:403-435/Domain: ankyrin repeat homology &lt;AN12&gt;

F:436-468/Domain: ankyrin repeat homology &lt;AN13&gt;

F:469-501/Domain: ankyrin repeat homology &lt;AN14&gt;

F:502-534/Domain: ankyrin repeat homology &lt;AN15&gt;

F:535-567/Domain: ankyrin repeat homology &lt;AN16&gt;

F:568-600/Domain: ankyrin repeat homology &lt;AN17&gt;

F:601-633/Domain: ankyrin repeat homology &lt;AN18&gt;

F:634-666/Domain: ankyrin repeat homology &lt;AN19&gt;

F:667-699/Domain: ankyrin repeat homology &lt;AN20&gt;

F:700-732/Domain: ankyrin repeat homology &lt;AN21&gt;

F:733-765/Domain: ankyrin repeat homology &lt;AN22&gt;

F:766-798/Domain: ankyrin repeat homology &lt;AN23&gt;

## Query Match

17.6%; Score 133.5; DB 2; Length 1856;

Best Local Similarity 35.4%; Pred. No. 0.00023;

Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;

8 LATAARGRVEERALLLEAVLALPNAPNSYGRRIQV-MMGSAFVAELLILHGAEPCAD 66

Db 507 LHIAARGHVEYVLLALLEKESQACMTKKGFTPLHVAATKYKRVALLERDANHPNAG 566

QY 67 PATLTPVNDAREGFLDTL-VVLRAGARLDVDDAW-GRLPVDLAEELGHRDVARYL-- 122

Db 567 KNGILT-PLHVAVHNHNDIVKLLPRGGS--PHSPAMNGYTPRLHIAKQNOVEVARSLQ 623

QY 123 ---RAAAGTGRGSNHRARIDAAGPSDI 146

Db 624 YGGSANAESVOGVTPRLHIAQEGHAEM 650

## RESULT 15

A35049

ankyrin 1, erythrocyte splice form 2 - human

N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N:Contains: ankyrin 2.2, erythrocyte

C:Species: Homo sapiens (man)

C:Date: 27-Jul-1990 #sequence\_revision 01-Oct-1992 #text\_change 04-Sep-1998

C:Accession: A35049

R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A:Title: cDNA sequence for human erythrocyte ankyrin.

A:Reference number: A35049; M0ID:90175370

A:Accession: A35049

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1880 &lt;LAN&gt;

A:Cross-references: GB:M28880

A:Gene: GDB:ANK1; ANK

A:Cross-references: GDB:118737; OMIM:182900

Map position: Bp11.2-Bp11.2

Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing; cytoskeleton

F:2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted &lt;MA1&gt;

F:2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted &lt;MA2&gt;

F:44-76/Domain: ankyrin repeat homology &lt;AN01&gt;

F:77-109/Domain: ankyrin repeat homology &lt;AN02&gt;

F:110-142/Domain: ankyrin repeat homology &lt;AN03&gt;

F:143-171/Domain: ankyrin repeat homology &lt;AN04&gt;

F:172-204/Domain: ankyrin repeat homology &lt;AN05&gt;

F:205-237/Domain: ankyrin repeat homology &lt;AN06&gt;

F:238-270/Domain: ankyrin repeat homology &lt;AN07&gt;

F:271-303/Domain: ankyrin repeat homology &lt;AN08&gt;

F:304-336/Domain: ankyrin repeat homology &lt;AN09&gt;

F:337-369/Domain: ankyrin repeat homology &lt;AN10&gt;

F:370-402/Domain: ankyrin repeat homology &lt;AN11&gt;

F:403-435/Domain: ankyrin repeat homology &lt;AN12&gt;

F:436-468/Domain: ankyrin repeat homology &lt;AN13&gt;

F:469-501/Domain: ankyrin repeat homology &lt;AN14&gt;

F:502-534/Domain: ankyrin repeat homology &lt;AN15&gt;

F:535-567/Domain: ankyrin repeat homology &lt;AN16&gt;

F:568-600/Domain: ankyrin repeat homology &lt;AN17&gt;

F:601-633/Domain: ankyrin repeat homology &lt;AN18&gt;

F:634-666/Domain: ankyrin repeat homology &lt;AN19&gt;

F:667-699/Domain: ankyrin repeat homology &lt;AN20&gt;

F:700-732/Domain: ankyrin repeat homology &lt;AN21&gt;

F:733-765/Domain: ankyrin repeat homology &lt;AN22&gt;

F:766-798/Domain: ankyrin repeat homology &lt;AN23&gt;

## Query Match

17.6%; Score 133.5; DB 2; Length 1880;

Best Local Similarity 35.4%; Pred. No. 0.00024;

Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;

8 LATAARGRVEERALLLEAVLALPNAPNSYGRRIQV-MMGSAFVAELLILHGAEPCAD 66

Db 507 LHIAARGHVEYVLLALLEKESQACMTKKGFTPLHVAATKYKRVALLERDANHPNAG 566

QY 67 PATLTPVNDAREGFLDTL-VVLRAGARLDVDDAW-GRLPVDLAEELGHRDVARYL-- 122

Db 567 KNGILT-PLHVAVHNHNDIVKLLPRGGS--PHSPAMNGYTPRLHIAKQNOVEVARSLQ 623

QY 123 ---RAAAGTGRGSNHRARIDAAGPSDI 146

Db 624 YGGSANAESVOGVTPRLHIAQEGHAEM 650

Search completed: September 19, 2002, 17:24:24  
Job time: 83 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:23:41 ; Search time 11.84 Seconds

(without alignments)  
483.994 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 760

Sequence: 1 MEPSADWLATTAARGRVEFV.....TRGSNHARTDAEGPSDIPD 148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753	99.1	156	1	CDN2_HUMAN
2	529	69.6	130	1	CDN5_MOUSE
3	524	68.9	130	1	CDN5_MOUSE
4	522	68.7	138	1	CDN5_MOUSE
5	461.5	60.7	167	1	CDN5_MOUSE
6	408	53.7	171	1	CDN2_MONDO
7	259	34.1	166	1	CDN7_HUMAN
8	249	32.8	166	1	CDN7_MOUSE
9	231.5	30.5	168	1	CDN6_MOUSE
10	228.5	30.1	168	1	CDN6_MOUSE
11	158	20.8	3924	1	ANK2_HUMAN
12	137.5	18.1	1862	1	ANK2_MOUSE
13	133.5	17.6	768	1	YB23_HUMAN
14	133.5	17.6	1880	1	ANK1_HUMAN
15	130.5	17.2	1431	1	DAPK_HUMAN
16	125	16.4	1964	1	NTC4_MOUSE
17	123	16.2	1059	1	Y379_HUMAN
18	118.5	15.6	347	1	GABG_MOUSE
19	118.5	15.6	382	1	GABG_MOUSE
20	117.5	15.5	347	1	GABG_HUMAN
21	117.5	15.5	383	1	GABG_HUMAN
22	114	15.0	768	1	BARI_RAT
23	114	15.0	2437	1	NOTC_BRARE
24	113	14.9	437	1	V014_FOWPV
25	111.5	14.7	2531	1	NTC1_RAT
26	111	14.6	333	1	ANKH_CHRVI
27	111	14.6	777	1	BARI_HUMAN
28	110.5	14.5	2444	1	NTC1_HUMAN
29	109.5	14.4	832	1	ANK2_HUMAN
30	107.5	14.1	592	1	V246_FOWPV
31	107	14.1	765	1	BARI_MOUSE
32	106.5	14.0	2703	1	NOTC_MOUSE
33	104.5	13.8	2524	1	NOTC_XENLA

34	103.5	13.6	2318	1	NTC3_MOUSE
35	102.5	13.5	740	1	Y050_HUMAN
36	100.5	13.2	414	1	GABD_MOUSE
37	100.5	13.2	500	1	CACT_DROME
38	100.5	13.2	1178	1	P811_YEAST
39	100	13.2	668	1	V244_FOWPV
40	99.5	13.1	1454	1	KDGE_DROME
41	98	12.9	708	1	G1T2_MOUSE
42	96.5	12.7	461	1	V218_FOWPV
43	96.5	12.7	605	1	GLSL_CAEEL
44	96	12.6	603	1	V162_FOWPV
45	96	12.6	735	1	RNSA_MOUSE

## ALIGNMENTS

RESULT	ID	CDN2_HUMAN	STANDARD	PRT	156 AA.
AC	P42771	O15191			
DT	01-NOV-1995	(Rel. 32, Created)			
DT	15-JUL-1998	(Rel. 41, Last sequence update)			
DT	01-MAR-2002	(Rel. 41, Last annotation update)			
DE	Cyclin-dependent kinase 4 inhibitor A (CDK4i) (P16-INK4) (P16-INK4A)				
DE	(Multiple tumor suppressor 1) (MTS1).				
GN	CDKN2A OR CDKN2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=94081956; PubMed=8259215;				
RT	Serrano M., Hannon G.J., Beach D.;				
RT	"A new regulatory motif in cell-cycle control causing specific				
RT	inhibition of cyclin D/CDK4."				
RL	Nature 366:704-707(1993).				
RN	(2)				
RP	SEQUENCE OF 51-152 FROM N.A.				
RA	MEDLINE=94204645; PubMed=8153634;				
RA	Kamb A., Guis N.A., Weaver-Feldhaus J., Liu Q., Harsman K.,				
RA	Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,				
RT	Skolnick M.H.;				
RT	"A cell cycle regulator potentially involved in genesis of many tumor				
RT	types."				
RL	Science 264:436-440(1994).				
RN	(3)				
RP	SEQUENCE OF 1-20 FROM N.A.				
RA	MEDLINE=96182088; PubMed=8622687;				
RA	Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;				
RT	"Regulation of p16CDKN2 expression and its implications for cell				
RT	immortalization and senescence."				
RL	Mol. Cell. Biol. 16:859-867(1996).				
RN	(4)				
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.				
RA	MEDLINE=98421670; PubMed=9751050;				
RA	Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;				
RT	"Structural basis for inhibition of the cyclin-dependent kinase Cdk6				
RT	by the tumour suppressor p16INK4a."				
RL	Nature 395:237-243(1998).				
RN	(5)				
RP	STRUCTURE BY NMR.				
RA	MEDLINE=20027100; PubMed=10559205;				
RA	Yuan C., Li J., Seldy T.L., Byeon I.J., Tsai M.D.;				
RT	"Tumor suppressor INK4: comparisons of conformational properties				
RT	between p16(INK4A) and p18(INK4C)."				
RL	J. Mol. Biol. 294:201-211(1999).				
RN	(6)				
RP	REVIEW ON MELANOMA VARIANTS.				
RA	MEDLINE=96377761; PubMed=8783570;				
RA	Dracopoli N.C., Fountain J.W.;				
RT	"CDKN2 mutations in melanoma."				

RL Cancer Surv. 26:115-132(1996).  
 RN [7]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=96303699; PubMed=8723678;  
 RA Smit-Scoerensen B., Hovig E.;  
 RT "CDKN2A (p16INK4A) somatic and germline mutations.";  
 RL Hum. Mutat. 7:294-303(1996).  
 RN [8]  
 RP VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).  
 RX MEDLINE=94338323; PubMed=8060323;  
 RA Hayashi N., Sugimoto Y., Tsuchiya F., Ogawa M., Nakamura Y.;  
 RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41  
 (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small  
 cell lung carcinomas.";  
 RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).  
 RN [9]  
 RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 AND  
 RP THR-148.  
 RX MEDLINE=95078916; PubMed=7987387;  
 RA Hussussian C.J., Struwing J.P., Goldstein A.M., Haggins P.A.T.,  
 Ally D.S., Sheehan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;  
 RT "Germline p16 mutations in familial melanoma.";  
 RL Nat. Genet. 8:15-21(1994).  
 RN [10]  
 RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.  
 RX MEDLINE=95060835; PubMed=7970734;  
 RA Zhou X., Tarrin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,  
 RA Abraham J.M., Meltzer S.J.;  
 RT "The MTS1 gene is frequently mutated in primary human esophageal  
 tumors.";  
 RL Oncogene 9:3737-3741(1994).  
 RN [11]  
 RP VARIANTS.  
 RX MEDLINE=95188190; PubMed=7882351;  
 RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,  
 RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zaritska M.,  
 RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;  
 RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in  
 primary and metastatic lung cancer.";  
 RL Cancer Res. 55:1448-1451(1995).  
 RN [12]  
 RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.  
 RX MEDLINE=96121580; PubMed=8395405;  
 RA Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,  
 RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;  
 RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma  
 kindreds.";  
 RL Hum. Mol. Genet. 4:1845-1852(1995).  
 RN [13]  
 RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 AND  
 T-148.  
 RX MEDLINE=95375774; PubMed=7647780;  
 RA Renade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,  
 RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,  
 RA Dracopoli N.C.;  
 RT "Mutations associated with familial melanoma impair p16INK4  
 function.";  
 RL Nat. Genet. 10:114-116(1995).  
 RN [14]  
 RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68, T-85 AND T-148.  
 RX MEDLINE=96323259; PubMed=8710906;  
 RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., MacDonald D.J.,  
 RA Luchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,  
 RA Iselbacher K.J., Sober A.J., Haber D.A.;  
 RT "Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in  
 familial melanoma: analysis of a clinic-based population.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).  
 RN [15]  
 RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.  
 RX MEDLINE=97472457; PubMed=9328469;  
 RA Harland M., Meloni R., Gruis N., Plinney E., Brookes S., Spurr N.K.,  
 RA Fritschauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,  
 RA Bishop D.J., Bishop J.N.;

RT "Germline mutations of the CDKN2 gene in UK melanoma families.";  
 RL Hum. Mol. Genet. 6:2061-2067(1997).  
 RN [16]  
 RP VARIANTS FAMILIAL MELANOMA.  
 RX MEDLINE=96087572; PubMed=9425228;  
 RA Soultir N., Avril M.-F., Chompret A., Demenais F., Bombléd J.,  
 RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Pallieres B.;  
 RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone  
 families in France.";  
 RL Hum. Mol. Genet. 7:209-216(1998).  
 RN [17]  
 RP ERRATUM.  
 RA Soultir N., Avril M.-F., Chompret A., Demenais F., Bombléd J.,  
 RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Pallieres B.;  
 RL Hum. Mol. Genet. 7:941-941(1998).  
 RN [18]  
 RP VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.  
 RA Grelandsdottir S., Olafsdottir G.H., Borg A.;  
 RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,  
 RT glioma and carcinoma of the pancreas.";  
 RL Hum. Mutat. 12:212-212(1998).  
 RN [19]  
 RP VARIANTS MELANOMA GLY-59; TYR-84; TRP-87 AND TRP-101.  
 RX MEDLINE=20332815; PubMed=10874641;  
 RA Ruiz A., Pulig S., Malvey J., Lazaro C., Lynch M., Gimenez-Arnau A.M.,  
 RA Pulig L., Sanchez-Coronejo J., Estivill X., Castel T.;  
 RT "CDKN2A mutations in Spanish cutaneous malignant melanoma families and  
 RT patients with multiple melanomas and other neoplasia.";  
 RL J. Med. Genet. 36:480-493(1999).  
 CC -I- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS  
 CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE  
 CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.  
 CC -I- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.  
 CC -I- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A  
 CC WIDE RANGE OF TISSUES.  
 CC -I- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 CC INHIBITORS.  
 CC -I- SIMILARITY: CONTAINS 4 ANK REPEATS.  
 CC -----  
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 CC -----  
 DR EMBL: L27211; AAA92554.1; -;  
 DR EMBL: U12820; AAB60645.1; -;  
 DR EMBL: U12819; AAB60645.1; JOINED.  
 DR EMBL: U12819; AAB60645.1; JOINED.  
 DR EMBL: S69804; AAD14048.1; -;  
 DR EMBL: X94154; CAA63870.1; -;  
 DR PDB: 1B17; 16-FEB-99.  
 DR PDB: 1DC2; 23-DEC-99.  
 DR MIM: 600160; -;  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 3.  
 DR PROSITE: PS50088; ANK\_REPEAT; FALSE\_NEG.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;  
 KW Polymorphism; Li-Fraumeni syndrome; 3D-structure.  
 FT REPEAT 11 40 ANK 1.  
 FT REPEAT 44 72 ANK 2.  
 FT REPEAT 77 106 ANK 3.  
 FT REPEAT 110 139 ANK 4.  
 FT REPEAT 14 14 ANK 4.  
 FT VARIANT D->E (IN A BILARY TRACT TUMOR).  
 FT /FTid=VAR\_001408.  
 FT VARIANT 16 16 L->P (IN A BILARY TRACT TUMOR AND A  
 FT FAMILIAL MELANOMA).  
 FT /FTid=VAR\_001409.  
 FT A->P (IN A LUNG TUMOR AND MELANOMA).  
 FT /FTid=VAR\_001410.

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Query Match          99.1%; Score 753; DB 1; Length 156;
Best Local Similarity 99.3%; Pred. No. 1.2e-65;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSAWMLTAARGVEEYRALLEVALPNAPNNSYGRPPIOVMGMSARVAELLILHGA 60
    |||
DB 9 MESSAWMLTAARGVEEYRALLEVALPNAPNNSYGRPPIOVMGMSARVAELLILHGA 68
    |||

QY 61 EPNCADPATITRPVHDAAREGFLDTLVLRAGARLDVDAWGRLPVDAEEELGHRDVAR 120
    |||
DB 69 EPNCADPATITRPVHDAAREGFLDTLVLRAGARLDVDAWGRLPVDAEEELGHRDVAR 128
    |||

QY 121 YLRAAAGTRGSHARIDAEGPSDIPD 148
    |||
DB 129 YLRAAAGTRGSHARIDAEGPSDIPD 156
    |||

RESULT 2
CT MOUSE STANDARD; PRT; 130 AA.
AC P55271;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95380169; PubMed=7651726;
RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
RL Oncogene 11:635-645(1995).

RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J X DBA;
RX MEDLINE=97322242; PubMed=9178896;
RA Melumbres M., de Castro I., Santos J., Melendez B., Mangues R.,
RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
RT "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by
RT deletion and de novo methylation with independence of p16INK4a
RT alterations in murine primary T-cell lymphomas.";
RI Oncogene 14:1361-1370(1997).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC -1- POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED UBICITOUSLY.
CC -1- INDUCTION: BY TGF-BETA.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
CC -----
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CC -----
DB EMBL: U66085; AAB39833.1;
DB EMBL: U66084; AAB39833.1; JOINED.
DB HSSP: P42771; 1B17.
DB MGD: MGI:104737; Cdkn2b.
DB InterPro: IPR002110; ANK.
DB Pfam: PF00023; ank. 3.
DB SMART: SM00248; ANK. 1.

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DR PROSITE; PSS0088; ANK_REPEAT. 1.
DR PROSITE; PSS0297; ANK_REPEAT_REGION. 1.
KW Cell Cycle; Anti-oncogene; Repeat; ANK repeat.
FT REPEAT 5 34 ANK 1.
FT REPEAT 38 66 ANK 2.
FT REPEAT 71 100 ANK 3.
FT REPEAT 104 130 ANK 4.
SQ SEQUENCE 130 AA; 1378 MW; 7AAD60FF52BCFF9 CRC64;

Query Match          69.6%; Score 529; DB 1; Length 130;
Best Local Similarity 88.3%; Pred. No. 3.4e-44;
Matches 106; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 8 LATAARGVEEYRALLEVALPNAPNNSYGRPPIOVMGMSARVAELLILHGAEPNCADP 67
    |||
DB 10 LATAARGVEEYRALLEVALPNAPNNSYGRPPIOVMGMSARVAELLILHGAEPNCADP 69
    |||

QY 68 ATLTPRVHDAAREGFLDTLVLRAGARLDVDAWGRLPVDAEEELGHRDVAR 127
    |||
DB 70 ATLTPRVHDAAREGFLDTLVLRAGARLDVDAWGRLPVDAEEELGHRDVAR 129
    |||

RESULT 3
CDN5_RAT STANDARD; PRT; 130 AA.
AC P55272;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B).
GN CDKN2B OR INK4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96001392; PubMed=7546221;
RA Hino O., Kobayashi E., Hirayama Y., Kubo Y.,
RA Tsuchiya H., Kikuchi Y., Mitani H.;
RT "Molecular genetic basis of renal carcinogenesis in the Eker rat
RT model of tubercular sclerosis (Tsc2).";
RL Mol. Cellinog. 14:23-27(1995).

RN [2]
RP SEQUENCE OF 46-86 FROM N.A.
RX MEDLINE=95228036; PubMed=7712460;
RA Knapek D.F., Serrano M., Beach D., Trono D., Walker C.L.;
RT "Association of rat p15INK4b/p16INK4 deletions with monosomy 5 in
RT kidney epithelial cell lines but not primary renal tumors.";
RL Cancer Res. 55:1607-1612(1995).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC -1- POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN
CC TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL
CC KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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DB EMBL: S79760; AAB35360.1;

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DR EMBL: S77734.1; NOT_ANNOTATED.CDS.
DR HSSP: Q60773.1AP7.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 3.
DR SMART: SM00248; ANK; 1.
DR PROSITE: PSS0088; ANK_REPEAT; 1.
DR PROSITE: PSS0297; ANK_REPEAT_REGION; 1.
DR Cell cycle; Anti-oncogene; Repeat; 1.
KW CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT CHAIN 1 130
FT LONG ISOFORM
FT CHAIN 46 130
FT CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT INT_MET 46 46
FT REPEAT 5 34
FT REPEAT 38 66
FT REPEAT 71 100
FT REPEAT 104 130
FT ANK 4.
SQ SEQUENCE 130 AA; 13748 MW; AC45B21FA69FAD92 CRC64;

Query Match
Best Local Similarity 68.9%; Score 524; DB 1; Length 130;
Matches 104; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 8 LATTAAGRGVEVRALLLEAVLPNAPNSYGRPIQYMMGSAVAVALLLHGAEPCADP 67
DB 10 LATTAAGRGVEYRQLEELAGADPNVAVRFGRRPIQYMMGSAVAVALLLHGAEPCADP 69
QY 68 ATLTPRVPHDARREGFDLTIVLHRAGARLDVPRAMGRPLPYDLAEELGHNDVAVYLRAAAG 127
DB 70 ATLTPRVPHDARREGFDLTIVLHRAGARLDVPRAMGRPLPYDLAEELGHNDVAVYLRAAAG 129

RESULT 4
ID CDN5_HUMAN STANDARD; PRT; 138 AA.
AC P42772;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin-dependent kinase 4 inhibitor B (P16-INK4B) (P15-INK4B)
DE (Multiple tumor suppressor 2) (MTS2).
GN CDKN2B OR MTS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RA MEDLINE=95095079; PubMed=8001816;
RA Guan K.-L., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
RA Matera G.A., Xiong Y.;
RT "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related
RT CDK6 inhibitor, correlates with wild-type p53 function.";
RL Genes Dev. 8:2939-2952(1994).
RN [2]
RS SEQUENCE FROM N.A.
RA MEDLINE=94359613; PubMed=8078588;
RA Hannon G.J., Beach D.;
RT "p13INK4B is a potential effector of TGF-beta-induced cell cycle
RT arrest.";
RL Nature 371:257-261(1994).
RN [3]
RS SEQUENCE OF 53-138 FROM N.A.
RA MEDLINE=94204645; PubMed=8153634;
RA Kamd A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
RA Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
RA Skolnick M.H.;
RT "A cell cycle regulator potentially involved in genesis of many tumor
RT types";
RL Science 264:436-440(1994).
RN [4]
RS VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50.

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RX MEDLINE=95188190; PubMed=7882351;
RA Okamoto A., Hussain S.P., Hagihara K., Spillare E.A., Rusin M.R.,
RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zaritawa M.,
RA Xiong Y., Beach D.H., Yokota J., Harris C.C.;
RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in
RT primary and metastatic lung cancer.";
RL Cancer Res. 55:1448-1451(1995).
CC -! FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC -! POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST.
CC -! SUBUNIT: HETERODIMER OF P14 WITH CDK4.
CC -! DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
CC -! SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -! SIMILARITY: CONTAINS 2 ANK REPEATS.
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CC -----
DR EMBL: U17075; AAC50075.1; -
DR EMBL: L36844; AAA50282.1; -
DR EMBL: S69805; AAD14049.1; -
DR HSSP: P42771; 1B17.
DR MIM: 600431; -
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 3.
DR PROSITE: PSS0088; ANK_REPEAT; FALSE_NEG.
DR PROSITE: PSS0297; ANK_REPEAT_REGION; 1.
KW Cell cycle; Anti-oncogene; Repeat; 1.
KW Cell cycle; Anti-oncogene; Repeat; 1.
FT REPEAT 13 39
FT REPEAT 73 103
FT VARIANT 47 47
FT VARIANT 50 50
FT VARIANT 50 50
FT CONFLICT 20 21
FT CONFLICT 23 23
FT CONFLICT 32 34
SQ SEQUENCE 138 AA; 14722 MW; 0D6FBDFA6FEAD21 CRC64;

Query Match
Best Local Similarity 68.7%; Score 522; DB 1; Length 138;
Matches 106; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 4 SADWLATAAGRGVEVRALLLEAVLPNAPNSYGRPIQYMMGSAVAVALLLHGAEPCN 63
DB 14 SDEGLASAAAGRGVEYRQLEELAGADPNVAVRFGRRPIQYMMGSAVAVALLLHGAEPCN 73
QY 64 CADPATLTPRVPHDARREGFDLTIVLHRAGARLDVPRAMGRPLPYDLAEELGHNDVAVYLR 123
DB 74 CADPATLTPRVPHDARREGFDLTIVLHRAGARLDVPRAMGRPLPYDLAEELGHNDVAVYLR 133
QY 124 AAAG 127
DB 134 TATG 137

RESULT 5
ID CDN2_MOUSE STANDARD; PRT; 167 AA.
AC P51480;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin-dependent kinase 4 inhibitor A (CDK4i) (P16-INK4) (P16-INK4A).
GN CDKN2A OR P16INK4A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95380169; PubMed=7651726;
RA Queller D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
RT Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
RL "Cloning and characterization of murine p16INK4 and p15INK4b genes.";
CC Oncogene 11:635-645(1995).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE
CC PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6.
CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES
CC CONTAINED CDK6.
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L76150; AAA85453.1; -
DR HSSP: Q60773; 1AP7.
DR MGD: MGI:104736; Cdkn2a.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 3.
DR SMART: SM00248; ANK; 1.
DR PROSITE: PS50088; ANK_REPEAT; FALSE_NEG.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
KW CHAIN 1 167
FT CHAIN 1 167
FT FT 43 167 LONG ISOFORM.
FT FT 43 167 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
FT REPEAT 43 167 SHORT ISOFORM.
FT REPEAT 35 63 FOR SHORT ISOFORM.
FT REPEAT 101 130 ANK 1.
FT REPEAT 101 130 ANK 2.
SQ SEQUENCE 167 AA; 17870 MW; 88C4588A105ECB8F CRC64;

Query Match 60.7%; Score 461.5; DB 1; Length 167;
Best Local Similarity 63.2%; Pred. No. 1.4e-37;
Matches 98; Conservative 16; Mismatches 32; Indels 9; Gaps 3;

OY 1 MESPADMLAARAAAGRGVEEYRALLEVALPNAFNSYGRPIQVMMGSAVVAELLHGA 60
DB 1 MESADMLA-RAAOGRVHADVALLACVSPNAPNSFGKPTIQVMGNNVAVALLNTGA 59
OY 61 EPNCADPATLTFRVHDARREGFLDTLVVLRAGARLDVDRDAMGRLPVDIAEELGHRDVAR 120
DB 60 DSNCEDEPTFSRPVHDARREGFLDTLVVLRHSGARLDVDRDAMGRRLPDLAQRGHQDIYR 119
OY 121 YLRAA-----AGGT--RGSNHAIRIDAEGPSDIP 147
DB 120 YLRSAGCSLCSAGWSLCTAGNAVQDGHSPSSSTP 154

RESULT 6
ID CDN2_MONDO STANDARD; PRT; 171 AA.
AC 077617;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin-dependent kinase 4 inhibitor A (CDK4I) (P16-INK4) (P16-INK4A)

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DE (Tumor suppressor CDKN2A).
GN CDKN2A.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxId=13616;
RN [1]
RP SEQUENCE FROM N.A.
RX Sherburn T.E., Gale J.M., Ley R.D.;
RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 3 ANK REPEATS.
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CC -----
DR EMBL: AF064808; AAC23669.1; -
DR EMBL: AF064808; AAC23670.1; -
DR HSSP: P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 3.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
KW CHAIN 1 171
FT CHAIN 1 171
FT FT 35 171 LONG ISOFORM.
FT FT 35 171 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
FT REPEAT 45 74 SHORT ISOFORM.
FT REPEAT 78 106 FOR SHORT ISOFORM.
FT REPEAT 111 140 ANK 1.
FT REPEAT 111 140 ANK 2.
FT REPEAT 111 140 ANK 3.
SQ SEQUENCE 171 AA; 18707 MW; 694264F5D04F6CC CRC64;

Query Match 53.7%; Score 408; DB 1; Length 171;
Best Local Similarity 69.2%; Pred. No. 2e-32;
Matches 83; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

OY 4 SADWLATAAARGVEEYRALLEVALPNAFNSYGRPIQVMMGSAVVAELLHGAEPN 63
DB 46 SGEKLTAAARGRTVEVLELLELGTNPANVRFGHSAIQVMMGNNVAVALLIYGAEPN 105
OY 64 CADPATLTFRVHDARREGFLDTLVVLRAGARLDVDRDAMGRLPVDIAEELGHRDVAR 123
DB 106 TDDPTTLTLPVHDARREGFLDTLVVLRHSGARLDVDRDAMGRRLPDLAQRGHQDIYR 165

RESULT 7
ID CDN7_HUMAN STANDARD; PRT; 166 AA.
AC P55273; Q13102;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cyclin-dependent kinase 4 inhibitor D (P19-INK4D).
GN CDKN2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;

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DR      MIM: 600927; -.
DR      InterPro: IPR002110; ANK.
DR      Pfam: PF000023; ank, 3.
DR      SMART: SM00248; ANK, 1.
DR      PROSITE: PS50088; ANK_REPEAT, 1.
DR      PROSITE: PS50297; ANK_REPEAT_REGION, 1.
KM      Cell cycle: Anti-oncogene; Repeat; ANK repeat; 3D-structure.
FT      REPEAT       41        69          ANK 1.
FT      REPEAT       73       102          ANK 2.
FT      REPEAT       106       135          ANK 3.
FT      REPEAT       138       166          ANK 4.
FT      CONFLICT     159       159          Q -> P (IN REF. 2).
SQ      SEQUENCE     166 AA; 17700 MW; 2FACD1CFC56340DC CRC64;

Query Match           34.1%; Score 259; DB 1; Length 166;
Best Local Similarity 44.0%; Pred. No. 4e-18;
Matches   66; Conservative    18; Mismatches   60; Indels    6; Gaps    3

OY      4 SADMLTAARAAAGVEEVRALL-EAVLAPNAPNSGRPIQVMMGSAVARLELLHGAP 62
DB      8 AGRLSGAARGVQVEVKRLHRELHPDLNFEGTALQVMFGSTALALELKGGASP 67
OY      63 NCADPALTTPVHAAREGFELDTLVYLHRAGARDVDAMGRPLVDLAELGHRYARYL 122
DB      68 NMDITSG-TSPVIDARTGFLDTLKVLRHGAADVNPDPGTGALPHILAVQEGHTAVSFL 126
OY      123 RAAAG----GTGGSNHARIDAAEGPSDIPD 148
DB      127 AAESDLRRDARKGLPLEVALRGADLDVD 156

RESULT      8
CDNT_MOUSE ID CDNT_MOUSE STANDARD: PRT; 166 AA.
AC      060773; 060794;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Cyclin-dependent kinase 4 inhibitor D (P19-INK4D).
GN      CDKR2D.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL KAPLAN;
RX      MEDLINE=95257948; PubMed=7739547;
RA      Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;
RT      "Novel INK4 proteins, p19 and p18, are specific inhibitors of the
RL      cyclin D-dependent kinases CDK4 and CDK6."
RM      Mol. Cell. Biol. 15:2672-2681(1995).
[2]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=95257949; PubMed=7739548;
RA      Chan F.K.W., Zhang J., Cheng L., Shapiro D.N., Winoto A.;
RT      "Identification of human and mouse p19, a novel CDK4 and CDK6
RL      inhibitor with homology to p16ink4."
RM      Mol. Cell. Biol. 15:2682-2686(1995).
[3]
RP      STRUCTURE BY NMR.
RX      MEDLINE=98013176; PubMed=9353127;
RA      Luh F.Y., Archer S.J., Domaille P.J., Smith B.O., Owen D.,
RB      Brotherton D.H., Raine A.R., Xu X., Brizuela L., Brenner S.L.,
RA      Laue E.D.;
RT      "Structure of the cyclin-dependent kinase inhibitor p19ink4d.";
RL      Nature 389:999-1003(1997).
CC      -I- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
CC      -I- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC      INHIBITORS.
CC      -I- SIMILARITY: CONTAINS 3 ANK REPEATS.

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RX MEDLINE=96438606; PubMed=8840966;
RA Lapointe J., Lachance Y., Labrie Y., Labrie C.;
RT "A p18 mutant defective in CDK6 binding in human breast cancer
RL cells.";
RN Cancer Res. 56:4586-4589(1996).
[4]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
RX MEDLINE=98100086; PubMed=9437433;
RA Venkataraman R., Swaminathan K., Marmorstein R.;
RT "Crystal structure of the CDK4/6 inhibitory protein p18INK4c provides
RT insights into ankyrin-like repeat structure/function and
RL tumor-derived p18INK4 mutations.";
RN Nat. Struct. Biol. 5:74-81(1998).
[5]
RP STRUCTURE BY NMR.
RX MEDLINE=99175088; PubMed=10074345;
RA Li J., Byeon I.-J.L., Ericson K., Poi M.-J., O'Wallie P., Selby T.,
RA Tsai M.-D.;
RT "Tumor suppressor INK4: determination of the solution structure of
RT p18INK4c and demonstration of the functional significance of loops in
RT p18INK4c and p16INK4A.";
RN Biochemistry 38:2930-2940(1999).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
CC CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON
CC ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
CC -1- SUBUNIT: HETERODIMER OF P18 WITH CDK6.
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN SKELETAL MUSCLE. ALSO
CC FOUND IN PANCREAS AND HEART.
CC -1- DISEASE: CDKN2C MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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CC -----
DR EMBL: U17074; AAC50074.1; -
DR EMBL: AF041248; AAC39782.1; -
DR EMBL: AF041250; AAC39783.1; -
DR EMBL: AF041249; AAC39783.1; JOINED.
DR PDB: 1HB; 13-JAN-99.
DR PDB: 1B09; 13-SEP-99.
DR MIM: 603369; -
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 4.
DR SMART: SM00246; ANK; 2.
DR PROSITE: PS50088; ANK_REPEAT; 2.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Cell cycle; Repeat; Disease mutation; 3D-structure.
FT REPEAT 4 33 ANK 1.
FT REPEAT 37 65 ANK 2.
FT REPEAT 69 98 ANK 3.
FT REPEAT 102 132 ANK 4.
FT VARIANT 72 72 A -> P (IN BREAST CANCER; LOSS OF CDK6
FT INTERACTION).
FT FTID=VAR_001490.
SQ SEQUENCE 168 AA; 18127 MW; 5D66AFA715186E9A CRC64;
Query Match 30.1%; Score 228.5; DB 1; Length 168;
Best Local Similarity 40.3%; Pred. No. 3.5e-15;
Matches 56; Conservative 22; Mismatches 60; Indels 1; Gaps 1;
OY 2,EP5ADMLATAAARGVEEVALLAEVALPNAPNSYGRBPRIQVMMSARVALLDGLGAE 61
DB 3 EPMGNELSAARAGDLEQITSLQNNVNVNANONGFRTALQVMKLGNEIARRILLRGAN 62
OY 62 PNCADPATLTIRPVHDAARGFLDTLVVLRAGARLVDANGRLPVDLAEELGHRDVAR 121

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DB 63 PDLKD-RTGFATVHDAARGFLDTLTQTLLEFDADVIEDNEGNLPLHLAAREGHLRYVEF 121
OY 122 LRRAAGTGRGSHARIDAA 140
DB 122 LVKHTASNVGHRHKKGDTA 140
RESULT 11
ANK2_HUMAN STANDARD; PRT; 3924 AA.
ID ANK2_HUMAN
AC Q01484; Q01485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).
GN ANK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain stem;
RX MEDLINE=91302466; PubMed=1830053;
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
RT "Isolation and characterization of cDNAs encoding human brain
RT ankyrins reveal a family of alternatively spliced genes.";
RN J. Cell Biol. 114:241-253(1991).
[2]
RN REVISIONS.
RA Carpenter S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain stem;
RX MEDLINE=94075409; PubMed=8253844;
RA Chan W., Kordeli E., Bennett V.;
RT "440-kD ankyrin1: structure of the major developmentally regulated
RT domain and selective localization in unmyelinated axons.";
RN J. Cell Biol. 123:1463-1473(1993).
[4]
RN SEQUENCE OF 463-495 FROM N.A.
RX MEDLINE=9200921; PubMed=1833308;
RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
RA Lux S.E., Ward D.C., Forget B.G.;
RT "Isolation and chromosomal localization of a novel nonerythroid
RT ankyrin gene.";
RN Genomics 10:858-866(1991).
CC -1- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC elements. Also bind to cytoskeletal proteins.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2 AND 3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
CC CELLS THROUGHOUT THE BRAIN.
CC -1- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
CC AND FUNCTION (POTENTIAL).
CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56957; CAA40278.1; -
DR EMBL: X56958; CAA40279.2; -
DR EMBL: Z28634; CABA2644.1; -
DR EMBL: M37123; AAA62828.1; -

```

DR PIR: S14533; S14533.  
 DR PIR: B39643; B39643.  
 DR PIR: B39643; B39643.  
 DR PIR: S14569; S14569.  
 DR HSP: 000421; IAWC.  
 DR MIM: 106410; -.  
 DR InterPro: IPR002110; ANK.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR000906; ZUS.  
 DR Pfam: PF00023; ank; 24.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00791; ZUS; 1.  
 DR PRINTS: PRO1415; ANKYRIN.  
 DR SMART: SM00248; ANK; 21.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00218; ZUS; 1.  
 DR PROSITE: PS50088; ANK\_REPEAT; 20.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 DR K Cytokeleton: Alternative splicing; Repeat; ANK repeat;  
 K Phosphorylation.  
 FT REPEAT 63 92 ANK 1.  
 FT REPEAT 96 125 ANK 2.  
 FT REPEAT 129 158 ANK 3.  
 FT REPEAT 162 191 ANK 4.  
 FT REPEAT 193 220 ANK 5.  
 FT REPEAT 232 261 ANK 6.  
 FT REPEAT 265 294 ANK 7.  
 FT REPEAT 298 327 ANK 8.  
 FT REPEAT 331 360 ANK 9.  
 FT REPEAT 364 393 ANK 10.  
 FT REPEAT 397 426 ANK 11.  
 FT REPEAT 430 459 ANK 12.  
 FT REPEAT 463 492 ANK 13.  
 FT REPEAT 496 525 ANK 14.  
 FT REPEAT 529 558 ANK 15.  
 FT REPEAT 562 591 ANK 16.  
 FT REPEAT 595 624 ANK 17.  
 FT REPEAT 628 657 ANK 18.  
 FT REPEAT 661 690 ANK 19.  
 FT REPEAT 694 723 ANK 20.  
 FT REPEAT 727 756 ANK 21.  
 FT REPEAT 760 789 ANK 22.  
 FT REPEAT 793 822 ANK 23.  
 FT DOMAIN 1773 1950 REPEAT-RICH REGION.  
 FT REPEAT 1773 1784 REPEAT A.  
 FT REPEAT 1785 1796 REPEAT A.  
 FT REPEAT 1809 1820 REPEAT A.  
 FT REPEAT 1821 1832 REPEAT A.  
 FT REPEAT 1833 1844 REPEAT A.  
 FT REPEAT 1856 1867 REPEAT A.  
 FT REPEAT 1857 1867 REPEAT A (APPROXIMATE).  
 FT REPEAT 1868 1879 REPEAT A.  
 FT REPEAT 1891 1891 REPEAT A.  
 FT REPEAT 1892 1902 REPEAT A (APPROXIMATE).  
 FT REPEAT 1903 1914 REPEAT A.  
 FT REPEAT 1915 1926 REPEAT A.  
 FT REPEAT 1927 1938 REPEAT A.  
 FT REPEAT 1939 1950 REPEAT A.  
 FT DOMAIN 3536 3620 DEATH.  
 FT VARSPLIC 1039 1039  
 FT VARSPLIC 1444 3528  
 FT CONFLICT 475 476  
 FT CONFLICT 971 971  
 FT CONFLICT 3582 3582  
 FT CONFLICT 3586 3586  
 SO SEQUENCE 3924 AA; 430337 MW; 52AC496C428E29D2 CRC64;

Query Match 20.8%; Score 158; DB 1; Length 3924;  
 Best Local Similarity 37.2%; Pred. No. 7; le-07;

Matches 48; Conservative 18; Mismatches 59; Indels 4; Gaps 3;  
 QY 8 LATAARGVEVVALLEAVALPAPNSYGRPPQV-MMGSAVALLLLHCAEPNCAD 66  
 Db 468 LHMARAGQVEVNCVLLRNGALVDARREQTPHLASRLGKTEIYOLLQHNHADAAT 527  
 QY 67 PATLTPRVHDAAREGFLDTLVLRACARLDVDRDAMGRLPVDLAEEELGHDVARYL--RA 124  
 Db 528 TNGYT-PLHISARREGQVDVASVLLGGAHSLATKGFTHLVAAKGSIDVAKLLQRR 586  
 QY 125 AAGTSGSN 133  
 Db 587 AAADSAGKN 595  
 RESULT 12  
 ID ANK1\_MOUSE STANDARD; PRT; 1862 AA.  
 AC 002357;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Ankyrin 1 (Erythrocyte ankyrin).  
 GN ANK1 OR ANK-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Erythrocyte;  
 RX MEDLINE=92345717; PubMed=1386265;  
 RA White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;  
 "Murine erythrocyte ankyrin cDNA: highly conserved regions of the  
 regulatory domain.";  
 RL Mamm. genome 3:281-285(1992).  
 CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL  
 ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO  
 NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE  
 CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.  
 CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE  
 CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;  
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC  
 CC PLASMA MEMBRANE.  
 CC -1- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).  
 CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).  
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: M84756; AAA37236.1; -.  
 CC HSP: 000421; IAWC.  
 CC MGD: MGI:88024; Ank1.  
 DR InterPro: IPR002110; ANK.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR000906; ZUS.  
 DR Pfam: PF00023; ank; 23.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00791; ZUS; 1.  
 DR PRINTS: PRO1415; ANKYRIN.  
 DR SMART: SM00248; ANK; 22.  
 DR SMART: SM00005; DEATH; 1.  
 DR PROSITE: PS50088; ANK\_REPEAT; 20.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.

[illegible]

Query Match	17.6%	Score 133.5	DB 1	Length 766
Best Local Similarity	33.8%	Pred. No. 2.6e-05		
Matches	49	Conservative	14	Mismatches 75; Indels 7; Gaps 3;
QY	8	LATAAARGVEEYKALLENVALPNNAPNSYGRPIQV-MMGSAEYAEILLHGAEPNCAD	66	
DB	124	LTAASMGASVYNTLLEWGAVDSDISDCRGVLSIASAQGVVEVYRTLLDRGLDENHRD	183	
QY	67	PATLIRPVDAAREGFLLTLVLRAGARLDVDRDAGRPLVDAELGHRDVARYL----	122	
DB	184	DAGWI-PLHMAFEGHRLCEALIDGAGTANTIDDRIPFLASQEGHYDCVQLLENK	242	
QY	123	-RAAAGTRGSNHARIDAEGPSDI	146	
DB	243	SNIDRGYDGRNALRYAALEGHRDI	267	
RESULT	14			
ANK1_HUMAN				
TD	ANK1_HUMAN	STANDARD:	PRT:	1880 AA.
AC	P16157;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DE	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Ankyrin 1 (Erythrocyte ankyrin) (Ankyrin R).			
GN	ANK1 OR ANK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.			
RC	TISSUE=Hematopoietic;			
RX	MEDLINE=90158830; PubMed=2137557;			

RA Lux S.E., John K.M., Bennett V.;  
 RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated  
 RT structure with homology to tissue-differentiation and cell-cycle  
 RT control proteins.";  
 RL Nature 344:36-42(1990).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90175370; PubMed=169849;  
 RA Lambert S., Yu H., Pichal J.T., Lawler J., Ruff P., Speicher D.,  
 RA Cheung M.C., Kan Y.W., Palek J.;  
 RT "cDNA sequence for human erythrocyte ankyrin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).  
 RN [3]  
 RP VARIANT HS IIE-462.  
 RX MEDLINE=96225450; PubMed=8640229;  
 RA Eder S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,  
 RA Dornwell M., Heiders J., Kugler M., Oezcan R., Pekrun A.,  
 RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;  
 RT "Ankyrin-1 mutations are a major cause of dominant and recessive  
 RT hereditary spherocytosis.";  
 RL Nat. Genet. 13:214-218(1996).  
 CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL  
 CC ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO  
 CC NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE  
 CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.  
 CC ERYTHROCYTE ANKIRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE  
 CC CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;  
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC  
 CC PLASMA MEMBRANE.  
 CC -1- ALTERNATIVE PRODUCTS: At least 3 isoforms: 1/2.1 (shown here),  
 CC 2/2.2 and 3: are produced by alternative splicing.  
 CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).  
 CC -1- DISEASE: Defects in ANK1 are the cause of dominant and recessive  
 CC hereditary spherocytosis (HS).  
 CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.  
 CC -----  
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 CC -----  
 CC DR EMBL, X16609; CAA34610.1; -;  
 CC DR EMBL, M28880; AAA51732.1; -;  
 CC DR EMBL, S08275; SJHK.  
 CC DR PIR, A35049; A35049.  
 CC DR HSP, G00421; IAWC.  
 CC DR MIM, 182900; -;  
 CC DR InterPro: IPR002110; ANK.  
 CC DR InterPro: IPR000488; Death.  
 CC DR InterPro: IPR000906; ZUS.  
 CC DR Pfam, PF00023; ank; 23.  
 CC DR Pfam, PF00531; death; 1.  
 CC DR Pfam, PF00791; ZUS; 1.  
 CC DR PRINTS: PR01415; ANKYRIN.  
 CC DR SMART, SM00248; ANK; 22.  
 CC DR SMART, SM00005; DEATH; 1.  
 CC DR SMART, SM00218; ZUS; 1.  
 CC DR PROSITE, PS50088; ANK\_REPEAT; 20.  
 CC DR PROSITE, PS50089; ANK\_REPEAT\_REGION; 1.  
 CC DR PROSITE, PS50017; DEATH\_DOMAIN; 1.  
 CC DR Cytoskeleton; Alternative splicing; Repeat; ANK repeat;  
 CC Phosphorylation; Lipoprotein; Disease mutation; Elliptocytosis;  
 CC Polymorphism.  
 CC KW INIT\_MET 0  
 CC FT DOMAIN 1 826 89 KDA DOMAIN (ANION EXCHANGE PROTEIN  
 CC BINDING DOMAIN).  
 CC FT DOMAIN 827 1381 62 KDA DOMAIN (SPECTRIN BINDING

FT DOMAIN 1382 1880 DOMAIN)  
 FT 55 KDA REGULATOR DOMAIN (REGULATES  
 FT THE BINDING OF ANKYRIN TO SPECTRIN  
 FT AND THE BAND 3 PROTEIN).  
 FT REPEAT 43 72 ANK 1.  
 FT REPEAT 76 105 ANK 2.  
 FT REPEAT 109 138 ANK 3.  
 FT REPEAT 142 171 ANK 4.  
 FT REPEAT 173 200 ANK 5.  
 FT REPEAT 204 233 ANK 6.  
 FT REPEAT 237 266 ANK 7.  
 FT REPEAT 270 299 ANK 8.  
 FT REPEAT 303 332 ANK 9.  
 FT REPEAT 336 365 ANK 10.  
 FT REPEAT 369 398 ANK 11.  
 FT REPEAT 402 431 ANK 12.  
 FT REPEAT 435 464 ANK 13.  
 FT REPEAT 468 497 ANK 14.  
 FT REPEAT 501 530 ANK 15.  
 FT REPEAT 534 563 ANK 16.  
 FT REPEAT 567 596 ANK 17.  
 FT REPEAT 600 629 ANK 18.  
 FT REPEAT 633 662 ANK 19.  
 FT REPEAT 666 695 ANK 20.  
 FT REPEAT 699 728 ANK 21.  
 FT REPEAT 732 761 ANK 22.  
 FT REPEAT 765 794 ANK 23.  
 FT DOMAIN 1402 1486 MISSING (IN ISOFORM 2).  
 FT VARSPPLIC 1512 1873 H -> D (IN ISOFORM 2).  
 FT VARSPPLIC 1874 1874 TVEGLEPSELEVDIDYEMKSHKDHSTPNP -> ELKGS  
 FT VARSPPLIC 1849 1880 GLOPDLLEGKKGQIVKRSKLRGKQ (IN ISOFORM  
 FT 3).  
 FT R -> T.  
 FT /FTID=VAR\_000595.  
 FT V -> I (IN HS).  
 FT /FTID=VAR\_000596.  
 FT R -> H (IN BRUGEN).  
 FT /FTID=VAR\_000597.  
 FT V -> A.  
 FT /FTID=VAR\_000598.  
 FT D -> E.  
 FT /FTID=VAR\_000599.  
 FT E -> D.  
 FT /FTID=VAR\_000601.  
 FT S -> T.  
 FT /FTID=VAR\_000600.  
 FT D -> N (IN DDESSELDORF).  
 FT /FTID=VAR\_000602.  
 FT R -> D.  
 FT /FTID=VAR\_000603.  
 FT A -> S (IN REF. 2).  
 FT V -> I (IN REF. 2).  
 FT CONFLICT 229 229  
 FT CONFLICT 1545 1545  
 FT SO SEQUENCE 1880 AA; 206145 MW; 1C5F5E7EFD1CD428 CRC64;  
 Query Match 17.6%; Score 133.5; DB 1; Length 1880;  
 Best Local Similarity 35.4%; Pred. No. 7.1e-05;  
 Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;  
 QY 8 LATAAAGRVEEVALLEAVALPNAFNSYGRPIQV-MMMGSAKVALLLLHGAERPCAD 66  
 DB LHIARSGHVEETVALLEKEASQCKRTKFTPLHVAKYGVAVALLLERRDHPNAAG 565  
 QY 67 PATLTPRVNDAAREGFDTL-VVLRAGARLDVDAW-GRLPVDALEELGRDVARYL-- 122  
 DB 566 KNGLT-PLHVAVHNNDIYKLLPRGGS--PHSPRANGTTPHLIAKQNOVVAASLID 622  
 QY 123 ---RAAGGTGSHNARIIDAEGPSDI 146  
 DB 623 YGGSANNAESVGVTPPLHIAAGGHAEH 649

```

RESULT 15
DAPK_HUMAN STANDARD; PRT; 1431 AA.
ID DAPK_HUMAN
AC P53355;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Death-associated protein kinase 1 (EC 2.7.1.-) (DAP kinase 1).
GN DAPK1 OR DAPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95129831; Pubmed=7828849;
RA Deiss L.P., Feinstein E., Berissi H., Cohen O., Klinchi A.;
RT "Identification of a novel serine/threonine kinase and a novel 15-KD
RT protein as potential mediators of the gamma interferon-induced cell
RT Death.";
PM Genes Dev. 9:15-30(1995).
[2]
RP REVISIONS TO 164-171.
RA Feinstein E.;
RU Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
CC DEATH.
CC -1- PTM: AUTOPHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 10 ANK REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X76104; CAA53712.1; -.
CC HSSP: 063450; 1A06.
DR DR
DR MIM: 600831; -.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00023; ank; 8.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00248; ANK; 7.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS50088; ANK_REPEAT; 6.
DR PROSITE: PS50287; ANK_REPEAT_REGION; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
FT DOMAIN 13 266
FT 267 334 CALMODULIN-BINDING.
FT REPEAT 378 407 ANK 1.
FT REPEAT 411 440 ANK 2.
FT REPEAT 444 473 ANK 3.
FT REPEAT 478 507 ANK 4.
FT REPEAT 511 540 ANK 5.
FT REPEAT 544 573 ANK 6.
FT REPEAT 577 606 ANK 7.
FT REPEAT 610 639 ANK 8.
FT REPEAT 676 905 ANK 9.
FT REPEAT 1163 1197 ANK 10.

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FT DOMAIN 1313 1397 DEATH.
FT NP_BIND 19 27 ATP (BY SIMILARITY).
FT BINDING 42 42 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MUTAGEN 42 42 K->A: LOSS OF ACTIVITY.
SQ SEQUENCE 1431 AA; 160017 MW; 9EB84B11004A155B CRC64;

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Query Match 17.2%; Score 130.5; DB 1; Length 1431;
Best Local Similarity 29.1%; Pred. No. 0.0001;
Matches 44; Conservative 14; Mismatches 54; Indels 39; Gaps 4;

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QY 8 LATAAARGVEEVRALAEVALPNAPNISGRPRPQVMMSGAR----VAELLHLGAEPN 63
DB 483 LHCAAMHGYSYAKALCEAGCNVNINKNEGEP--LLTASARGYHDIVECLAEGADLN 539
QY 64 CADP-----ATL-----TRPVADAREGFLDTLVYVLR 91
DB 540 ACDDKDHIALHLAVARRCOMVEIKTLLSGCFVDYQDRHNTPLHVACKDGMPIVALCE 599
QY 92 AGARLDVDRDANGRLPVDLAEEIGHRDVARYL 122
DB 600 ANCNLDISNKYGRTPPLHLAANNGLIDVRYL 630

```

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Search completed: September 19, 2002, 17:27:22
Job time: 221 sec

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GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: September 19, 2002, 17:24:02 : Search time 26.94 Seconds  
(without alignments)  
950.380 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 760  
Sequence: 1 MEPSADWLATAAARGRYEV.....TRGSNHARIDAEGPSDIPD 148

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeop:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	72.1	106	4 Q9NP05	Q9NP05 homo sapien
2	512	67.4	130	11 Q91YF9	Q91YF9 mesocricetu
3	510	67.1	157	11 Q9E033	Q9E033 mesocricetu
4	501	65.9	144	11 Q99PH0	Q99PH0 mesocricetu
5	476.5	62.7	159	11 Q9R023	Q9R023 rattus norv
6	476	62.6	168	11 P97510	P97510 mus musculu
7	474	62.4	168	11 Q89088	Q89088 mus musculu
8	449	59.1	102	6 Q9XS51	Q9XS51 felis silve
9	444	58.4	103	6 Q9TSY1	Q9TSY1 sus scrofa
10	427	56.2	86	6 Q9XS52	Q9XS52 felis silve
11	409	53.8	81	6 Q9GMR2	Q9GMR2 canis famli
12	408	53.7	86	11 Q900P0	Q900P0 mus musculu
13	408	53.7	86	11 Q9ZIC1	Q9ZIC1 mus musculu
14	407	53.6	86	6 Q9TSY0	Q9TSY0 sus scrofa
15	405	53.3	86	11 Q54846	Q54846 mus musculu
16	334	43.9	113	11 Q9ZIC2	Q9ZIC2 mus musculu

17	331	43.6	113	11 Q9QWH5	Q9QWH5 mus musculu
18	327	43.0	113	11 Q9QWH8	Q9QWH8 mus musculu
19	326	42.9	113	11 Q9QWH7	Q9QWH7 mus musculu
20	326	42.9	113	11 Q9QWH6	Q9QWH6 mus musculu
21	314.5	41.4	112	11 Q9QWH4	Q9QWH4 mus musculu
22	292	38.4	124	13 P70067	P70067 xiphophorus
23	290	38.2	124	13 Q9W618	Q9W618 xiphophorus
24	282	37.1	124	13 Q9DE56	Q9DE56 fugu rubrip
25	264.5	34.8	164	13 Q9DES3	Q9DES3 fugu rubrip
26	254	33.4	166	11 Q91YV3	Q91YV3 mus musculu
27	234	30.8	58	6 Q97886	Q97886 equus cabal
28	231.5	30.5	168	11 Q9D153	Q9D153 mus musculu
29	209	27.5	116	4 Q95440	Q95440 homo sapien
30	157	20.7	843	11 P97582	P97582 rattus norv
31	149.5	19.7	1101	4 Q9NXY9	Q9NXY9 homo sapien
32	146	19.2	1166	4 Q9H2K2	Q9H2K2 homo sapien
33	146	19.2	1265	4 Q9H4S4	Q9H4S4 homo sapien
34	142	18.7	42	11 Q9ZIE8	Q9ZIE8 mus musculu
35	138	18.2	1136	6 Q9N180	Q9N180 bos taurus
36	137.5	18.1	1098	11 Q61304	Q61304 mus musculu
37	137.5	18.1	1848	11 Q61302	Q61302 mus musculu
38	137	18.0	299	11 Q91WK7	Q91WK7 mus musculu
39	137	18.0	300	4 Q9UGV1	Q9UGV1 homo sapien
40	137	18.0	40	4 Q95271	Q95271 homo sapien
41	136	17.9	1327	4 Q9ZIC3	Q9ZIC3 mus musculu
42	134.5	17.7	782	4 Q9BZ14	Q9BZ14 homo sapien
43	134.5	17.7	968	5 Q9VCM6	Q9VCM6 drosophila
44	134	17.6	1181	5 Q9XZ37	Q9XZ37 drosophila
45	134	17.6	1181	5 Q9VBP3	Q9VBP3 drosophila

## ALIGNMENTS

RESULT	ID	Q9NP05	PRELIMINARY:	PRT:	106 AA.
Q9NP05	Q9NP05	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	CDK41 PROTEIN (FRAGMENT).				
GN	CDK41.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=94203288; PubMed=8152487;				
RA	Nobori T., Miura K., Wu D.J., Lois A., Takabayashi K., Carson D.A.;				
RT	"Deletions of the cyclin-dependent kinase-4 inhibitor gene in multiple human cancers."				
RT	human cancers."				
RL	Nature 368:753-756(1994).				
DR	EMBL: S69824; AAD14050.1; .				
DR	EMBL: S69822; AAD14050.1; JOINED.				
DR	HSSP: P42771; 1B17.				
DR	InterPro: IPR002110; ANK.				
DR	PROSITE: PS50297; ANK_REPEAT_REGION; 1.				
KW	ANK repeat; Repeat.				
FT	NON_TER				
SO	SEQUENCE				
		106 AA;	11314 MW;	2D59442F956B6A61 CRC64;	

Query Match 72.1%; Score 548; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. NO. 2.3e-39;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	43	VMMGSRVAEILLHGAPNCADPATLTPYHDAAREGFLTLVILHRAGARLDVRAWM 102
DB	1	VMMGSRVAEILLHGAPNCADPATLTPYHDAAREGFLTLVILHRAGARLDVRAWM 60
QY	103	GRUPVLAERIGHRDVARYLRAAAGCTGSGNHARIDAEGPSDIPD 148

Db 61 GRPVDLAEBLGHVARYLRAAGGTGCSNHRIDAEGSPDIPD 106

## RESULT 2

Q91PF9 PRELIMINARY: PRT: 130 AA.

AC Q91PF9; 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE P15INK4B CYCLIN-DEPENDENT KINASE INHIBITOR.  
 GN P15INK4B.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 NC NCBL\_TaxID-10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE-PANCREAS;  
 RA Muscarella P., Ulrich A.B., Casto B.C., Montaux N., Knobloch T.J.,  
 Witel U.A., Melvin S., Pour P.M., Song H., Gold B., Batra S.K.,  
 Weghorst C.M.;  
 RT "Homologous Deletion of p15INK4b/p16INKA Gene Locus in Syrian Golden  
 Hamster Tumor Cell Lines."  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ302037; CAC67498.1; -  
 KW Kinase; Cyclin.  
 SQ SEQUENCE 130 AA; 13842 MW; 4C04DD3F8C6FE013 CRC64;

Query Match 67.4%; Score 512; DB 11; Length 130;

Best Local Similarity 85.0%; Pred. No. 3.3e-36;

Matches 102; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 8 LATRAARGVEEYRALLLEVALPNAPNSTGRPIQVMMGSAKYAEILLHGAEPNCADP 67  
 DB 10 LATRAARGVEEYRALLLEVALPNAPNSTGRPIQVMMGSAKYAEILLHGAEPNCADP 69  
 QY 68 ATLTREPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAELGHRDVARYRAAG 127  
 DB 70 NTLTREPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAELGHRDVARYRAAG 129

## RESULT 3

Q9E033 PRELIMINARY: PRT: 157 AA.

Q9E033; 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR 2.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 NC NCBL\_TaxID-10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Muscarella P., Knobloch T.J., Weghorst C.M.;  
 RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and  
 Identification of Inactivating Alterations in Hamster Tumor Cell  
 Lines."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF292567; AAG44950.1; -  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR SMART: SM00248; ANK; 4.  
 DR PROSITE: PS00297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 SQ SEQUENCE 157 AA; 16635 MW; 06FD66AEB6B30DC9F CRC64;

Query Match 67.1%; Score 510; DB 11; Length 157;  
 Best Local Similarity 68.9%; Pred. No. 6e-36;  
 Matches 102; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 1 MEPSADMLATAARGVEEYRALLLEVALPNAPNSTGRPIQVMMGSAKYAEILLHGA 60  
 DB 1 MEPSADGLARAAAGREGEVRLLEAGVSPNAPNCFGRTPIQVMMGNTQVARRLLLYGA 60  
 QY 61 EPNCAADPATLTREPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAELGHRDVAR 120  
 DB 61 EPNCEADPATLTSPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAELGHRDVAR 120  
 QY 121 YLRAAAGTGRGSHNRIDAEGSPDIPD 148  
 DB 121 YLRAAGNTPQSGSEPPAGVTSAGTPPEVSD 148

## RESULT 4

Q99PHO PRELIMINARY: PRT: 144 AA.

AC Q99PHO; 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DE CYCLIN-DEPENDENT CELL CYCLE INHIBITOR (FRAGMENT).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 NC NCBL\_TaxID-10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Muscarella P., Knobloch T.J., Weghorst C.M.;  
 RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and  
 Identification of Inactivating Alterations in Hamster Tumor Cell  
 Lines."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF291998; AAG59801.1; -  
 DR EMBL: AF291997; AAG59801.1; JOINED.  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR SMART: SM00248; ANK; 4.  
 DR PROSITE: PS00297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Repeat.  
 FT NON\_TER 144  
 SQ SEQUENCE 144 AA; 15206 MW; 8904FP9C0C316A084 CRC64;

Query Match 65.9%; Score 501; DB 11; Length 144;  
 Best Local Similarity 70.6%; Pred. No. 3.2e-35;  
 Matches 101; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 MEPSADMLATAARGVEEYRALLLEVALPNAPNSTGRPIQVMMGSAKYAEILLHGA 60  
 DB 1 MEPSADGLARAAAGREGEVRLLEAGVSPNAPNCFGRTPIQVMMGNTQVARRLLLYGA 60  
 QY 61 EPNCAADPATLTREPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAELGHRDVAR 120  
 DB 61 EPNCEADPATLTSPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAELGHRDVAR 120  
 QY 121 YLRAAAGTGRGSHNRIDAEGSP 143  
 DB 121 YLRAAGNTPQSGSEPPAGVTSAGTP 143

## RESULT 5

Q9R023 PRELIMINARY: PRT: 159 AA.

AC Q9R023; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)





OY 121 YLRAA-----AGCT--RGSNHARIDAEGPSDIP 147  
 Db 121 YLRSAGCSLCSAGWSLCTAGNVAQTGDGHSPSSSTP 155

RESULT 7  
 ID 089088 PRELIMINARY; PRT; 168 AA.

AC 089086;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).  
 GN CDKN2A OR E1ALPHA OR P16.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]

SEQUENCE FROM N.A.  
 STRAIN=BALB/CANPT; TISSUE=SPLEEN;  
 MEDLINE=98151529; PubMed=9482902;  
 RA Zhang S., Ramsay E.S., Mock B.A.;  
 RT "cdk2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and p19ARF, is a candidate for the plasmacytoma susceptibility locus, Pctrl.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).  
 RN [2]

SEQUENCE OF 1-42 FROM N.A.  
 RP STRAIN=MA/MAJ;  
 RC MEDLINE=97179476; PubMed=9021155;  
 RX Herzog C.R., You W.;

RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor suppressor gene."  
 RL Mamm. Genome 8:65-66(1997).  
 RN [3]

SEQUENCE OF 1-42 FROM N.A.  
 RC STRAIN=BALB/CJ AND MUS MUS POSCHIAVINUS;  
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M., Pellicer A., Fernandez-Piqueras J.;  
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains";  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF044335; AAC008962.1; -;  
 DR EMBL; U99279; AAC00051.1; -;  
 DR EMBL; U79626; AAD00224.1; -;  
 DR HSSP; P42771; 1B17.

MCD; MGI:104738; Cdkn2a.  
 InterPro: IPR002110; ANK.

Pfam: PF00023; ANK; 4.  
 SMART: SM00248; ANK; 1.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Cyclin; Kinase; Repeat.  
 SO SEQUENCE 168 AA; 17915 MW; 356A973BEAC4D167 CRC64;

Query Match 62.4%; Score 474; DB 11; Length 168;  
 Best Local Similarity 63.2%; Pred. No. 7.3e-33;  
 Matches 98; Conservative 17; Mismatches 32; Indels 8; Gaps 2;

OY 1 MESSAWMTAAARGVEYRALLLEVALPAPNSTGRPTIOWMMGSAARVAELLHGA 60  
 Db 1 MESAARLRRAAAGRVPRVRLLEAGVSPNAPNSFRPTIOWMMGNVHIALLLNCA 60

OY 61 EPNCADPATITRPVHDAREGFLDTLVVLRAGARLDVVDAGGRLPVDAEELGRDVAR 120  
 Db 61 DSNCEPPTTFSRPVHDAAEGFLDTLVVLRHGGARLDVVDAGGRLPDLAQRGHQDIVR 120

OY 12L YLRAA-----AGGT--RGSNHARIDAEGPSDIP 147  
 Db 121 YLRSAGCSLCSAGWSLCTAGNVAQTGDGHSPSSSTP 155

RESULT 8  
 ID 09XS51 PRELIMINARY; PRT; 102 AA.

AC 09XS51;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE P16/CDKN2A/MTS1 (FRAGMENT).  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_Taxid=9685;  
 RN [1]

SEQUENCE FROM N.A.  
 RP TISSUE=PERIPHERAL BLOOD;  
 RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y., Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;  
 RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A) and p15(MTS2/CDKN2B).";  
 RL EMBL; AB010807; BAA33540.1; -;  
 DR HSSP; P42771; 1B17

DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ANK; 3.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Repeat.  
 FT NON\_TER 1  
 FT NON\_TER 102  
 SQ SEQUENCE 102 AA; 10824 MW; 26399FF21359F35D CRC64;

Query Match 59.1%; Score 449; DB 6; Length 102;  
 Best Local Similarity 86.0%; Pred. No. 5.5e-31;  
 Matches 86; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

OY 43 YMMGSAARVAELLHLHGAEPNCADPATITRPVHDAREGFLDTLVVLRAGARLDVVDAM 102  
 Db 1 YMMGSAARVAELLHLHGAEPNCADPATITRPVHDAREGFLDTLVVLRAGARLDVVDAM 60

OY 103 GRLPYDLAEELGHRDVARVLRAGAGTGRGSHARIDAEG 142  
 Db 61 GRLPYDLAEERHNDIVRLARTRGTGSGSHGTGDAEG 100

RESULT 9  
 ID 09TSY1 PRELIMINARY; PRT; 103 AA.

AC 09TSY1;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR, P16 (FRAGMENT).  
 GN CDKN2A.

OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 OX NCBI\_Taxid=9823;  
 RN [1]

SEQUENCE FROM N.A.  
 RC STRAIN=LARGE WHITE;  
 RA Le Chalony C., Hayes H., Frelat G., Geoffroy C.;  
 RT "Identification and mapping of swine CDKN2A and CDKN2B exon2 sequences";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ242787; CAB65454.1; -;  
 DR HSSP; P42771; 1B17.

DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ANK; 2.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1  
 FT NON\_TER 103

SQ SEQUENCE 103 AA; 11023 MW; 5D23ABCC108BDE0B CRC64;  
 Query Match 58.4%; Score 444; DB 6; Length 103;  
 Best Local Similarity 84.3%; Pred. No. 1.5e-30;  
 Matches 86; Conservative 5; Mismatches 11; Indels 0; Gaps 0;  
 QY 43 VMMGSAVAVALLLHGAEPCADPATLTTPVHDAREGFLDTLVYLHRAGARLDVDRAM 102  
 Db 1 VMMGSAVAVALLLHGADPCADPATLTTPVHDAREGFLDTLVYLHRAGARLDVDRAM 60  
 QY 103 GRLPVDLAELGHRDVARYLRAAAGSTRGSNHAIRDAAGPS 144  
 Db 61 GRLPVDLAEEGRHVDVAGYLRANAGRTGGSNARSNGEDPA 102  
 RESULT 10  
 Q9XS52 PRELIMINARY; PRT; 86 AA.  
 Q9XS52:  
 01-NOV-1999 (Tremblrel. 12, Created)  
 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE p15/MTS2/CDKN2B (FRAGMENT).  
 OS Felis silvestris catus (cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PERIPHERAL BLOOD;  
 RA Okada M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,  
 RA Nishiyaki K., Watari T., Tsujimoto H., Hasegawa A.,  
 RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)  
 RT and p15(MTS2/CDKN2B)."  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB010808; BAA3541.1; -  
 DR HSSP: PA2771; 1B17  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 2.  
 DR PROSITE: PS50297; ANK\_REGION; 1.  
 DR ANK repeat; Repeat.  
 FT NON\_TER 1  
 SQ SEQUENCE 86 AA; 9340 MW; A59F0193290E867 CRC64;  
 Query Match 56.2%; Score 427; DB 6; Length 86;  
 Best Local Similarity 97.6%; Pred. No. 3.3e-29;  
 Matches 83; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 43 VMMGSAVAVALLLHGAEPCADPATLTTPVHDAREGFLDTLVYLHRAGARLDVDRAM 102  
 Db 1 VMMGSAVAVALLLHGADPCADPATLTTPVHDAREGFLDTLVYLHRAGARLDVDRAM 60  
 QY 103 GRLPVDLAELGHRDVARYLRAAAG 127  
 Db 61 GRLPVDLAEEGRHVDVARYLRAAAG 85  
 RESULT 11  
 Q9GMF2 PRELIMINARY; PRT; 81 AA.  
 Q9GMF2:  
 01-MAR-2001 (Tremblrel. 16, Created)  
 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE 4/6 INHIBITOR-A (FRAGMENT).  
 OS Canis familiaris (dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Venkataraj V.S., Mayor J., Modiano J.F.,  
 RT "Role of p16/INK4a in familial canine cancers."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF234176; AAG01087.1; -  
 DR HSSP: PA2771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR PROSITE: PS50297; ANK\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1  
 FT NON\_TER 81  
 SQ SEQUENCE 81 AA; 8868 MW; 0E39D8D05BAC0F CRC64;  
 Query Match 53.8%; Score 409; DB 6; Length 81;  
 Best Local Similarity 98.8%; Pred. No. 1e-27;  
 Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 43 VMMGSAVAVALLLHGAEPCADPATLTTPVHDAREGFLDTLVYLHRAGARLDVDRAM 102  
 Db 1 VMMGSAVAVALLLHGAEPCADPATLTTPVHDAREGFLDTLVYLHRAGARLDVDRAM 60  
 QY 103 GRLPVDLAELGHRDVARYL 122  
 Db 61 GRLPVDLAELGHRDVARYL 80  
 RESULT 12  
 Q9QUP0 PRELIMINARY; PRT; 86 AA.  
 Q9QUP0:  
 01-MAY-2000 (Tremblrel. 13, Created)  
 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
 GN p15.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VARIOUS STRAINS;  
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
 RA Pellicer A., Fernandez-Piqueras J.,  
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
 RT in mouse inbred strains."  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U79639; AAD00234.1; -  
 DR EMBL: U79636; AAD00232.1; -  
 DR EMBL: U79638; AAD00233.1; -  
 DR HSSP: PA2771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR PROSITE: PS50297; ANK\_REGION; 1.  
 DR ANK repeat; Cyclin; Kinase; Repeat.  
 FT NON\_TER 1  
 FT NON\_TER 86  
 SQ SEQUENCE 86 AA; 9269 MW; 509DB3613251B18 CRC64;  
 Query Match 53.7%; Score 408; DB 11; Length 86;  
 Best Local Similarity 92.9%; Pred. No. 1.4e-27;  
 Matches 79; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 43 VMMGSAVAVALLLHGAEPCADPATLTTPVHDAREGFLDTLVYLHRAGARLDVDRAM 102  
 Db 1 VMMGSAVAVALLLHGAEPCADPATLTTPVHDAREGFLDTLVYLHRAGARLDVDRAM 60  
 QY 103 GRLPVDLAELGHRDVARYLRAAAG 127  
 Db 61 GRLPVDLAEEGRHDIARYLHAAG 85  
 RESULT 13

```

Q92IC1
ID Q92IC1 PRELIMINARY; PRT; 86 AA.
AC Q92IC1;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN P15(INK4B).
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains."
RT Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
HSSP; P42771; 1B17.
EMBL; U79637; AAC00237.1; -.
DR InterPro: IPR002110; ANK.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Kinase; Repeat.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9269 MW; 509D9B3613251B18 CRC64;

Query Match 53.7%; Score 408; DB 11; Length 86;
Best Local Similarity 92.9%; Pred. No. 1.4e-27;
Matches 79; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 43 VMMGSAVAVALLLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 102
DB 1 VMMGSAVAVALLLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 60

QY 103 GRLPVDLAELGHRDVARYLRAAG 127
DB 61 GRLPVDLAELGHRDVARYLRAAG 85

RESULT 14
Q9TSYO PRELIMINARY; PRT; 86 AA.
AC Q9TSYO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).
GN CDKN2B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LARGE WHITE;
RA MEDLINE=2029098; PubMed=10828598;
RA Le Chalony C., Hayes H., Frelat G., Geffroy C.;
RT "Identification and mapping of swine cyclin-dependent kinase inhibitor
RT CDKN2A and CDKN2B exon2 sequences."
RT Cytogenet. Cell Genet. 88:240-243(2000).
RL EMBL; AJ242788; CAB65455.1; -.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR Pfam; PF00023; ank; 2.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Kinase; Repeat.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9286 MW; 16EF7A223293CFC9 CRC64;

```

```

Query Match 53.6%; Score 407; DB 6; Length 86;
Best Local Similarity 92.9%; Pred. No. 1.7e-27;
Matches 79; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 43 VMMGSAVAVALLLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 102
DB 1 VMMGSAVAVALLLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 60

QY 103 GRLPVDLAELGHRDVARYLRAAG 127
DB 61 GRLPVDLAELGHRDVARYLRAAG 85

RESULT 15
Q5486 PRELIMINARY; PRT; 86 AA.
AC Q5486;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15(INK4B) (FRAGMENT).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA MEDLINE=99124385; PubMed=9927195;
RA Malumbres M., de Castro I.P., Santos J., Piqueras J.F., Pellicer A.;
RT "Hypemethylation of the cell cycle inhibitor p15INK4b 3'-untranslated
RT region interferes with its transcriptional regulation in primary
RT lymphomas."
RT Oncogene 18:385-396(1999).
RL EMBL; AF015460; AAB94534.1; -.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Kinase; Repeat.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9237 MW; 0499DB26144FB6DF CRC64;

```

```

Query Match 53.3%; Score 405; DB 11; Length 86;
Best Local Similarity 91.8%; Pred. No. 2.4e-27;
Matches 78; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 43 VMMGSAVAVALLLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 102
DB 1 VMMGSAVAVALLLHGAEPCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDDAW 60

QY 103 GRLPVDLAELGHRDVARYLRAAG 127
DB 61 GRLPVDLAELGHRDVARYLRAAG 85

```

Search completed: September 19, 2002, 17:27:56  
Job time: 234 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:23:01 : Search time 30.1 Seconds

(without alignments)  
546.144 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 760

Sequence: 1 MEPSADWLAAARGRVEEV.....TRGSNHARIDAEGRDIPD 148

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq\_032802.\*  
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2: /SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1984.DAT.\*  
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13: /SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1992.DAT.\*  
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22: /SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	760	100.0	148	AA81701	Multiple tumour su
2	760	100.0	148	AA80940	Human multiple tum
3	760	100.0	151	AA853401	Inhibitor of cycli
4	760	100.0	156	AA85116	Cell-cycle regulat
5	760	100.0	156	AA24741	Human INK-4 protei
6	760	100.0	156	AA188354	Human cell cycle r
7	760	100.0	391	AAW23534	CDK Inhibitory fus
8	760	100.0	391	AAW5094	Human p27-p16 fusl
9	760	100.0	391	AA197526	Human W3 protein s
10	760	100.0	391	AA196041	Antiproliferative
11	760	100.0	391	AA196068	Angiogenesis inhib

12	753	99.1	156	18	AA10627	Tumour suppressor
13	753	99.1	156	18	AA19251	Human multiple tum
14	753	99.1	156	19	AA174549	Amino acid sequenc
15	753	99.1	156	20	AA10524	Human MTS1 protein
16	753	99.1	156	20	AA10524	A human multiple t
17	753	99.1	156	21	AA15498	Human MTS1 protein
18	753	99.1	156	21	AA197524	Human p16 protein
19	753	99.1	156	21	AA196053	Human cyclin depen
20	753	99.1	156	21	AA196067	Human multiple tum
21	753	99.1	156	21	AA192921	Human multiple tum
22	753	99.1	156	21	AA191102	Human MTS1 protein
23	753	99.1	156	21	AA159415	Human multiple tum
24	753	99.1	156	21	AA154902	Human multiple tum
25	753	99.1	156	22	AA102122	Human multiple tum
26	753	99.1	156	22	AA101002	Protein encoded by
27	753	99.1	156	22	AA167334	Human Multiple Tum
28	753	99.1	156	22	AA16890	Human W9 protein s
29	753	99.1	228	21	AA197522	Antiproliferative
30	753	99.1	228	21	AA196051	Angiogenesis inhib
31	753	99.1	228	21	AA196078	Truncated p27/p16
32	753	99.1	237	20	AA195105	Human W9 protein s
33	753	99.1	237	21	AA197534	Antiproliferative
34	753	99.1	237	21	AA196049	Angiogenesis inhib
35	753	99.1	237	21	AA196076	Truncated p27/p16
36	753	99.1	252	20	AA195106	Human M10 protein
37	753	99.1	252	21	AA197535	Antiproliferative
38	753	99.1	252	21	AA196050	Angiogenesis inhib
39	753	99.1	252	21	AA196077	Secretable angio
40	753	99.1	323	21	AA196079	Truncated p27/p16
41	753	99.1	334	20	AA195103	Human W8 protein s
42	753	99.1	334	21	AA197532	Antiproliferative
43	753	99.1	334	21	AA196047	Angiogenesis inhib
44	753	99.1	334	21	AA196074	CDK inhibitory fus
45	753	99.1	365	18	AA123536	

#### ALIGNMENTS

RESULT 1	
AA81701	
ID	AA81701 standard; Protein: 148 AA.
XX	
AC	AA81701;
XX	
DT	08-MAY-1996 (first entry)
XX	
DE	Multiple tumour suppressor 1 (MTS1) polypeptide.
XX	
KW	Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
KW	predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW	pancreas; breast; thyroid.
XX	
OS	Homo sapiens.
XX	
PN	W09525813-A1.
XX	
PD	28-SEP-1995.
XX	
PF	17-MAR-1995; 95WO-US03537.
XX	
PR	01-JUN-1994; 94US-0251938.
PR	18-MAR-1994; 94US-0215482.
PR	18-MAR-1994; 94US-0215086.
PR	18-MAR-1994; 94US-0215087.
XX	14-APR-1994; 94US-0227369.
XX	
PA	(MYRI-) MYRIAD GENETICS INC.
XX	(UTAH) UNIV UTAH RES FOUND.
XX	
PI	Cannon-Albright LA, Kamb A, Skolnick MH;
XX	
DR	WPI; 1995-344626/44.

DR N-PSDB: AAT00736.  
 XX  
 PT Detecting polymorphism associated with cancer pre:disposition - also  
 PT DNA, vectors and host cells e.g. for gene or protein replacement  
 PT therapy and drug screening  
 XX  
 PS Example 8; Pages 92-93; 148pp; English.  
 XX  
 CC An individual can be diagnosed as having a predisposition to cancer  
 CC by detecting an alteration in the wild type multiple tumour  
 CC suppressor (MTS) gene, using gene probes which hybridise to the MTS1  
 CC gene ORF AAT00736 (which encodes AAR81701) mutant sequences AAT00749/50.  
 CC The above assay can also be used in the diagnosis and prognosis of  
 CC melanoma, lymphoma, leukaemia and pancreas, breast and thyroid  
 CC cancers, etc..  
 CC  
 XX  
 SQ Sequence 148 AA:

Query Match 100.0%; Score 760; DB 16; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 6,6e-83;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEPSADWLATTAARGVEEVRALEAVLAPNAPNSYGRPRIOYMMGASARVAELLHGA 60  
 Db 1 mepsadwlataaargveevrallaeavlpnapnsygrprlqymmgasarvae11llhga 60  
 OY 61 EPNCADPATLTPRVHDAREGFLDTLVVLRAGARLDVDMGRLPVDLAEEELGHRDVAR 120  
 Db 61 epncadpatltrpvhdaregfltdltvvlrhagardlvdmagr1pvdlaeeelghrdvar 120  
 OY 121 YLRRAAGGTRGSNHARIDAAEGPSDIPD 148  
 Db 121 ylrraaggtgrsnharidaaegpsdipd 148

## RESULT 2

AAR80940  
 ID AAR80940 standard; Protein: 148 AA.

AC AAR80940;

DT 03-MAY-1996 (first entry)

XX Human multiple tumour suppressor polypeptide, MTS1.

KM Multiple tumour suppressor; E1-alpha; diagnosis; cancer; leukaemia;  
 KM astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;  
 KM gene therapy; chronic.

XX Homo sapiens.

PN WO9525429-A1.

XX 28-SEP-1995.

PF 17-MAR-1995; 95WO-US03316.

XX 01-JUN-1994; 94US-0251938.

PR 18-MAR-1994; 94US-0214581.

PR 18-MAR-1994; 94US-0214582.

PR 14-APR-1994; 94US-0215088.

PR 18-MAR-1994; 94US-0227369.

PR 18-MAR-1994; 94US-0215086.

XX 18-MAR-1994; 94US-0215087.

PA (MYRI-) MYRIAD GENETICS INC.

XX Kamb A;

PI WPI: 1995-344401/44.

DR N-PSDB: AAO99158.

PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences  
 PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.  
 PT melanoma or leukaemia  
 PT  
 XX  
 PS Claim 5; Page 92-93; 156pp; English.  
 XX  
 CC Several multiple tumour suppressor (MTS) polypeptides have been  
 CC isolated and sequenced. This sequence is the MTS polypeptide MTS1  
 CC MTS polypeptide-encoding cDNAs and mutants of these are useful for  
 CC the diagnosis or prognosis of human cancer. Germ-line mutations of  
 CC MTS cDNAs can be used for diagnosing predisposition to melanoma,  
 CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's  
 CC lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus,  
 CC testis, kidney, stomach and rectum. The wild-type gene is useful  
 CC for gene therapy and MTS polypeptides may also be used for protein  
 CC replacement therapy. Also the polypeptides or cells contg. an  
 CC altered MTS gene are useful for screening for potential cancer  
 CC therapeutics.  
 CC  
 XX  
 SQ Sequence 148 AA:

Query Match 100.0%; Score 760; DB 16; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 6,6e-83;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEPSADWLATTAARGVEEVRALEAVLAPNAPNSYGRPRIOYMMGASARVAELLHGA 60  
 Db 1 mepsadwlataaargveevrallaeavlpnapnsygrprlqymmgasarvae11llhga 60  
 OY 61 EPNCADPATLTPRVHDAREGFLDTLVVLRAGARLDVDMGRLPVDLAEEELGHRDVAR 120  
 Db 61 epncadpatltrpvhdaregfltdltvvlrhagardlvdmagr1pvdlaeeelghrdvar 120  
 OY 121 YLRRAAGGTRGSNHARIDAAEGPSDIPD 148  
 Db 121 ylrraaggtgrsnharidaaegpsdipd 148

## RESULT 3

AAR53401  
 ID AAR53401 standard; Protein: 151 AA.

AC AAR53401;

DT 07-DEC-1994 (first entry)

XX Inhibitor of cyclin dependent kinase 4 (p16INK4).

KM Cyclin; cyclin dependent kinase; CDK; oncogene; cancer; leukaemia;  
 KM lymphoma; cell cycle; detection; identification; tumour virus;  
 KM proliferating cell nuclear antigen; subunit; complex.

XX Homo sapiens.

PN WO9409135-A.

XX 28-APR-1994.

PF 18-OCT-1993; 93WO-US09945.

PR 16-OCT-1992; 92US-0963308.

PR 17-DEC-1992; 92US-0991997.

XX (COLD-) COLD SPRING HARBOR LAB.

PA Beach DH, Xiong Y;

PI WPI: 1994-151320/18.

DR N-PSDB: AAO63491.

PT Detection of subunit components of cyclin complexes - used for  
 PT diagnosing transformation of a cell and developing inhibitors and

PT activators, partic for cancer treatment  
XX  
PS Claim 13; Page 40; 45pp; English.  
XX  
CC The cell cycle gene implicated most strongly in oncogenesis is the  
CC human cyclin D1. It is genetically linked to the bcl-1 oncogene, a  
CC locus activated by translocation to an immunoglobulin gene enhancer  
CC in some B-cell lymphomas and leukemias. D-type cyclin, cyclin  
CC dependent kinase (CDK), PCNA (proliferating cell nuclear antigen) and  
CC p21 (a 21 kDa polypeptide) exist in a quaternary complex that many  
CC combinatorial variations of the components e.g. cyclin D1 or D3 and  
CC CDK2, CDK4 and CDKs, assemble in vivo. Each quaternary complex may  
CC have a subtly different role in the cell cycle or in different cell  
CC types. Cellular transformation by DNA tumour viruses such as SV40  
CC is associated with selective subunit rearrangement of the cyclin D  
CC complexes. In virally transformed cells, CDK4 totally dissociates  
CC from cyclin, PCNA and p21 and becomes associated with a 16 kilodalton  
CC polypeptide (p16). This sequence, designated p16INK4, binds to and  
CC inhibits CDK4. p16INK4 was discovered to show many similarities to  
CC p16. Reagents, such as monoclonal antibodies, can be developed that  
CC recognise the interactions between the CDK's cyclins, PCNA and low  
CC molecular weight polypeptides and can therefore be used to identify  
CC the state of transformation of a cell.  
XX  
SQ Sequence 151 AA;  
  
Query Match 100.0%; Score 760; DB 15; Length 151;  
Best Local Similarity 100.0%; Pred. No. 6.8e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MEPSADWLATAAARGVEEVRALLLEAVALPNAAPNSYGRRPICQVMGSAARVAELLHLHGA 60  
Db 1 mepsadwlataaargveevrallleavallpnapsygrripqvmumgsarvae111llhga 60  
  
QY 61 EPNCADPATLTTRPVDAAREGFLDTLVTLHRAGARLDVRDAGRLPVDLAELGHRDVAR 120  
Db 61 epncadpatlttrpvdaaregflidtlvhlhragarldvrdawgrlrvdlaeelghrdvar 120  
  
QY 121 YLRAAAGTGRGSHARIDAEGRSDIPD 148  
Db 121 ylrtaaagtrgsharidaegrpsdipd 148  
  
RESULT 4  
AAR85116  
ID AAR85116 standard; Protein; 156 AA.  
XX  
XX AAR85116;  
XX  
DT 01-MAR-1996 (first entry)  
XX  
XX Cell-cycle regulatory protein p16.  
DE Cell-cycle regulatory protein p16.  
XX  
XX Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;  
KW CCR; cancer; cell proliferation.  
XX  
XX Homo sapiens.  
OS  
XX  
PN M09528483-A1.  
XX  
PD 26-OCT-1995.  
XX  
PF 14-APR-1995; 95WO-0504636.  
XX  
PR 29-NOV-1994; 94US-0346147.  
PR 14-APR-1994; 94US-0227371.  
PR 25-MAY-1994; 94US-0248812.  
PR 14-SEP-1994; 94US-0306511.  
XX  
XX (COLD-) COLD SPRING HARBOR LAB.  
PA Beach DH, Demetrick DJ, Hannon GT, Serrano M;  
XX  
PI

XX  
DR WPI; 1995-373798/48.  
DR N-PSDB; AAT02962.  
XX  
PT New cell cycle regulating proteins bind to cyclin dependent kinase  
PT and related nucleic acids, antibodies etc., used in diagnosis and  
PT therapy of abnormal cell proliferation, degeneration etc.  
XX  
XX Claim 1; Page 76-77; 109pp; English.  
XX  
CC The human cell-cycle regulatory (CCR) protein p16 (AAR85116) was  
CC obtd. by expression of a cDNA clone (AAT02962) isolated in a 2-hybrid  
CC screening assay. CCR p16 specifically inhibits the activity of  
CC cyclin-dependent kinases during various stages of the cell cycle,  
CC and can be used in the treatment and diagnosis of proliferative  
CC disorders.  
XX  
SQ Sequence 156 AA;  
  
Query Match 100.0%; Score 760; DB 16; Length 156;  
Best Local Similarity 100.0%; Pred. No. 7.1e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MEPSADWLATAAARGVEEVRALLLEAVALPNAAPNSYGRRPICQVMGSAARVAELLHLHGA 60  
Db 9 mepsadwlataaargveevrallleavallpnapsygrripqvmumgsarvae111llhga 68  
  
QY 61 EPNCADPATLTTRPVDAAREGFLDTLVTLHRAGARLDVRDAGRLPVDLAELGHRDVAR 120  
Db 69 epncadpatlttrpvdaaregflidtlvhlhragarldvrdawgrlrvdlaeelghrdvar 128  
  
QY 121 YLRAAAGTGRGSHARIDAEGRSDIPD 148  
Db 129 ylrtaaagtrgsharidaegrpsdipd 156  
  
RESULT 5  
AAY24741  
ID AAY24741 standard; Protein; 156 AA.  
XX  
XX AAY24741;  
XX  
DT 23-AUG-1999 (first entry)  
XX  
XX Human INK-4 protein p16.  
DE  
XX  
XX INK-4; p16; p15; p18; p19; CDK4; cell cycle regulatory protein;  
KW transgenic mouse; p16-INK4-a; carcinogen; anti-proliferative.  
XX  
XX Homo sapiens.  
OS  
XX  
PN US5919997-A.  
XX  
PD 06-JUL-1999.  
XX  
PF 04-APR-1996; 96US-0627610.  
XX  
PR 04-APR-1996; 96US-0627610.  
PR 18-NOV-1993; 93US-0154915.  
PR 14-APR-1994; 94US-0227371.  
PR 25-MAY-1994; 94US-0248812.  
PR 14-SEP-1994; 94US-0306511.  
PR 29-NOV-1994; 94US-0346147.  
PR 30-JUN-1995; 95US-0497214.  
PR 02-JAN-1996; 96US-0581918.  
XX  
XX (COLD-) COLD SPRING HARBOR LAB.  
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.  
XX  
XX Beach DH, DePinho RA, Serrano M;  
XX  
XX WPI; 1999-394656/33.







Db 244 mepsadwlataaargveevraalleavapnapnsygrripqymmgarsarvaei11llhga 303  
 Oy 61 EPNCAADPATLTRPVHDAAREGFLDTLVLRAGARLDVBDAMQRLPVDAEELGHRDVAR 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 304 epncadpatltrpvhdaaregfldtlvlrhagarldvrdawgrlpvdaeeighrtdvar 363  
 Oy 121 YLRAAGTGRGSHARIDAAEGPSDIPD 148  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 364 yltraagtgtrsharidaaegpsdipd 391

## RESULT 9

AAy97526 standard; Protein; 391 AA.

Id AAY97526  
 AC AAY97526;  
 XX 15-JAN-2001 (first entry)  
 DT  
 XX  
 XX Human W3 protein sequence.

Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;  
 adenovirus E4 protein; neoplasia; W3 protein.

Homo sapiens.

WO200052184-A1.

08-SEP-2000.

01-MAR-2000; 2000WO-US05350.

01-MAR-1999; 99US-0122974.

08-APR-1999; 99US-0128271.

09-APR-1999; 99US-0128515.

(CELL-) CELL GENESYS INC.

(MITO-) MITOTIX INC.

Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;

WPI: 2000-587315/55.

N-PSDB: AAA96923.

Example 1; Page 108-109; 126pp; English.

This sequence represents the human W3 protein.

The invention relates to a protein composition comprising a novel

purified chimeric cyclin dependent kinase inhibitor (CDK1) and a

purified adenovirus E4 protein. The compositions comprising the protein,

or the DNA encoding it are useful for treating neoplasias in animals. The

compositions also find use in assays to eliminate a specific

sub-population of cultured cells, to determine the susceptibility of

neoplastic cells to treatment with the compositions and also in assays to

synchronize cell growth in cultured cells.

Sequence 391 AA;

Query Match

Best Local Similarity 100.0%; Score 760; DB 21; Length 391;  
 Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 304 epncadpatltrpvhdaaregfldtlvlrhagarldvrdawgrlpvdaeeighrtdvar 363  
 Oy 121 YLRAAGTGRGSHARIDAAEGPSDIPD 148  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 364 yltraagtgtrsharidaaegpsdipd 391

## RESULT 10

AAy96041 standard; Protein; 391 AA.

Id AAY96041

AC AAY96041;  
 XX 05-DEC-2000 (first entry)  
 DT  
 XX  
 XX Antiproliferative p27-p16 fusion protein W3.

Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;

W3; human; smooth muscle cell; hyperproliferation; restenosis;

vasotropic; antiproliferative; gene therapy.

Homo sapiens.

Synthetic.

Key Location/Qualifiers

Peptide 1..7 /label= 6His\_tag

Protein 8..204 /label= p27

Peptide 205..219 /label= p16

Protein 239..391 /label= p16

WO200052159-A1.

08-SEP-2000.

28-FEB-2000; 2000WO-US04971.

01-MAR-1999; 99US-0122974.

05-NOV-1999; 99US-0163682.

09-DEC-1999; 99US-0457568.

(CELL-) CELL GENESYS INC.

(MITO-) MITOTIX INC.

McArthur J, Gyuris J, Finer M;

WPI: 2000-594183/56.

N-PSDB: AAA50488.

Example 1; Page 101-103; 126pp; English.

The present sequence is that of p27-p16 fusion protein W3 comprising

an N-terminal 6His tag, the human p27 protein (see AAY96052), a

(GlySer)3 hinge and the human p16 protein (see AAY96053). It is

encoded by a nucleic acid obtained by PCR amplification of p27 and

p16 DNAs using primers that also included codons for the tag/hinge

regions. A claimed method for inhibiting smooth muscle cell

hyperproliferation involves transducing smooth muscle cells with a

replication-deficient recombinant adenovirus that lacks functional

E1 and E4 regions, and comprises a transgene encoding a cyclin

dependent kinase inhibitor (CDK1). The CDK1 is selected from an

INK4 family protein such as human p16, a CIP/KIP family protein

such as p27, active fragments of these, or fusion proteins

comprising (active fragments of) an INK4 family protein and a

CIP/KIP family protein (see AAY96046 and AAY96049). The method is used

to inhibit mammalian smooth muscle cell hyperproliferation, induced

CC by injury caused by angioplasty, stent placement or vein  
CC engraftment. It is useful for treating vascular pathologies e.g.,  
CC restenosis. Also claimed are recombinant lentiviruses encoding  
CC CDKs.

XX Sequence 391 AA:

Query Match 100.0%; Score 760; DB 21; Length 391;  
Best Local Similarity 100.0%; Pred. No. 2.4e-82;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADMTATAARGVEVRALLPAPNSYGRPIQVMMGSAARYAELLILHGA 60  
DB 244 mepsadwltataargvevrallpnapnsygrripqymmsarvae11llhga 303  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDANGRLPVDLAEELGHRVAR 120  
DB 304 epncadpatltrpvhdaaregfldtlvvhragardvrdawgrlpvdlaeelghrdvar 363  
Q 121 YLRAAGTGRGSHARIDAAEGSPDIP 148  
DB 364 ylraagtgtrgsharidaaegspdip 391

RESULT 11

AA96068  
ID AAY96068 standard; Protein; 391 AA.

AC AAY96068;

DT 05-DEC-2000 (first entry)

DE Angiogenesis inhibitor (p27-p16 fusion) W3.

XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; INK4; p27; p16;  
KW human; angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
KW endometriosis; psoriasis; vascular retinopathy; cycostatic;  
KW antirheumatic; antirheumatic; gynaecological; antipsoriatic;  
KW antiproliferative; gene therapy.

XX OS Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..7 /label= 6His\_tag

FT Protein 8..204 /label= p27

FT Peptide 205..219 /label= p16

FT Protein 239..391 /label= p16

XX Protein

XX W0200052158-A1.

XX 08-SEP-2000.

XX 28-FEB-2000; 2000WO-US04970.

XX 01-MAR-1999; 99US-0122974.

XX 05-NOV-1999; 99US-0163682.

XX 09-DEC-1999; 99US-0457646.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX Patel S, Marchur J, Gyuris J;

XX WPI; 2000-565501/52.

XX N-PSDB; AAA50523.

XX Inhibiting angiogenesis and treating angiogenesis-associated

PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
PT cell with a recombinant virus having a transgene encoding a cyclin  
PT dependent kinase inhibitor

XX Example 1; Page 108-110; 138pp; English.

CC The present sequence is that of p27-p16 fusion protein W3  
CC comprising an N-terminal 6His tag, the human p27 protein (see  
CC AAY96066), a (GlySer)3 hinge, and the human p16 protein (see  
CC AAY96067). The fusion protein is encoded by a nucleic acid (see  
CC AAA50523) that was obtained by PCR amplification of human p27 and p16  
CC DNAs using primers that also included codons encoding the tag/hinge  
CC regions of the fusion protein. A claimed method for inhibiting  
CC angiogenesis involves transducing an epithelial cell with a  
CC transgene encoding a cell dependent kinase inhibitor (CDK1). The  
CC delivery system for the transgene is a liposome or a recombinant  
CC virus. The CDK1 is a protein of the CIP/KIP family such as p27, a  
CC protein of the INK4 family such as p16, active fragments of these  
CC proteins, or a fusion of 2 CDK1 proteins such as p27 and p16. The  
CC method is useful in treating conditions associated with angiogenesis,  
CC such as neoplasia, rheumatoid arthritis, endometriosis, psoriasis  
CC and vascular retinopathy (claimed). Alternatively, the transgene  
CC is delivered to an auxiliary cell, and is expressed by that cell  
CC such that the CDK1 is released into the blood and contacts the  
CC target epithelial cell. The p27-p16 fusion proteins interact with  
CC CDK4/cyclinD, CDK2/cyclinA and CDK2/cyclinE and inhibit cell cycle  
CC progression.

XX Sequence 391 AA:

Query Match 100.0%; Score 760; DB 21; Length 391;

Best Local Similarity 100.0%; Pred. No. 2.4e-82; Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADMTATAARGVEVRALLPAPNSYGRPIQVMMGSAARYAELLILHGA 60  
DB 244 mepsadwltataargvevrallpnapnsygrripqymmsarvae11llhga 303  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDANGRLPVDLAEELGHRVAR 120  
DB 304 epncadpatltrpvhdaaregfldtlvvhragardvrdawgrlpvdlaeelghrdvar 363  
QY 121 YLRAAGTGRGSHARIDAAEGSPDIP 148  
DB 364 ylraagtgtrgsharidaaegspdip 391

RESULT 12

AAW10627  
ID AAW10627 standard; Protein; 156 AA.

AC AAW10627;

DT 28-OCT-1997 (first entry)

DE Tumour suppressor p16.

XX Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;

XX cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;

XX anti-angiogenic activity; hyperproliferative disorder.

XX Homo sapiens.

XX W09703635-A2.

XX 06-FEB-1997.

XX 17-JUL-1996; 96WO-US11787.

XX 17-JUL-1995; 95US-0502881.

XX (TEXA ) UNIV TEXAS SYSTEM.

```

PR 14-APR-1994; 94US-0227369.
PR 01-JUN-1994; 94US-0251938.
PR 17-MAR-1995; 95WO-US03537.
XX
PA (MYRI-) MYRIAD GENETICS INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Cannon-Albright LA, Kamb A, Skolnick MH;
PI
DR WPI; 1997-258217/23.
DR N-PSDB; AAT72311.
XX
PT Human mutant multiple tumour suppressor gene sequences - for
PT production of recombinant mutant polypeptide(s)
XX
PS Claim 1; Columns 61-64; 72pp; English.
PS
CC The present sequence the human multiple tumour suppressor 1
CC (MSI) gene product, useful in cancer diagnosis.
CC
XX
SQ Sequence 156 AA;

Query Match 99.1%; Score 753; DB 18; Length 156;
Best Local Similarity 99.3%; Pred. No. 4,9e-82;
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 1 MEPSADWLTATAAARGVEEVRALLLEAVALLPNAFNSYGRPIQVMWGSARVAELLHGA 60
   |||
Db 9 mepsadwataaargveevrallleagalpnapsygrtptqvmwgsarvae11lhga 68

QY 61 EPNCDPATLTPRPVIDARREGFDITVYLHRAGARLDYROMAGRLPVDLAEELEHRYAR 120
   |||
Db 69 epncdpattltprpvndarregfdltlvvlhragarldvrdawgrtlpydlaeeleghrdvar 128

QY 121 YLRAAGCTRGSNHARIDMAAGPSDIPD 148
   |||
Db 129 yltraaggtgrgsnharidaaegpsdipd 156

RESULT 14
AAW74549
ID AAW74549 standard; Protein: 156 AA.
XX
AC AAW74549;
XX
DC 04-DEC-1998 (first entry)
XX
DE Amino acid sequence of multiple tumour suppressor 1.
XX
KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
KW somatic mutation; gene therapy.
XX
OS Homo sapiens.
XX
PN US5801236-A.
XX
PD 01-SEP-1998.
XX
PE 07-JUN-1995; 95US-0480810.
XX
PR 07-JUN-1995; 95US-0480810.
XX
PR 18-MAR-1994; 94US-0214582.
XX
PR 18-MAR-1994; 94US-0215086.
XX
PR 18-MAR-1994; 94US-0215087.
XX
PR 14-APR-1994; 94US-0227369.
XX
PR 01-JUN-1994; 94US-0251938.
XX
PR 17-MAR-1995; 95WO-US03516.
XX
(MYRI-) MYRIAD GENETICS INC.
PA
PA Kamb A;
XX
XX

```

DR WPI: 1998-494842/42.  
 DR N-PSDB; AAV53819.  
 XX  
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
 useful as hybridisation probes, primers and recombinant production  
 PT of MTS in the diagnosis and treatment of cancers related to MTS  
 PT mutation(s)  
 XX  
 PS Disclosure: Column 63-64; 73pp; English.  
 XX  
 CC This is the amino acid sequence of the multiple tumour suppressor 1  
 CC (MTS-1) protein, used in the method of the invention. The MTS gene  
 CC is useful in the diagnosis and prognosis of human cancer, e.g. by  
 CC standard nucleic acid hybridisation techniques, of patient samples. The  
 CC mutated sequences are those that are present in somatic mutations  
 CC of the gene in cancers. The vectors can be used for gene therapy  
 CC strategies to replace function of mutated protein in patients. These  
 CC can also be used to construct protein mimetics, also for therapeutic  
 CC strategies. In addition the expression constructs can also be used  
 CC for recombinant production of MTS. Recombinant MTS can be used to  
 CC screen for drugs to be used for cancer therapy, and the protein  
 CC itself may also be used to restore MTS function in a cell.  
 XX  
 SQ Sequence 156 AA:  
 Query Match 99.1%; Score 753; DB 19; Length 156;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-82;  
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MESPADWLATAAARGVEEVRALLLEAVLPNAPNSYGRPRIOVMGMSARVAETLLHGA 60  
 Db 9 mepsadwlataaargveevrallleagalpnapnsygrripqymmgssarvae1111hga 68  
 QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRDAMGRLPVDLAELGHRDVAR 120  
 Db 69 epncadpatltrpvhdaaregfldtlvvlhragarldvrdawgrlpvdlaeelghrdvar 128  
 QY 121 YLRAAGTGRGSHARIDAEGPSDIPD 148  
 Db 129 ylrraagtgrgsharidaegpsdipd 156  
 RESULT 15  
 ID AAM40524  
 XX AAM40524 standard; Protein; 156 AA.  
 AC AAM40524;  
 XX  
 DE 15-JUL-1998 (first entry)  
 XX  
 DE Human MTS1 protein.  
 XX  
 KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;  
 KW familial melanoma locus; MLM; predisposition.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5739027-A.  
 PD 14-APR-1998.  
 XX  
 PF 07-JUN-1995; 95US-0487033.  
 XX  
 PR 07-JUN-1995; 95US-0487033.  
 PR 18-MAR-1994; 94US-0214582.  
 PR 18-MAR-1994; 94US-0215086.  
 PR 18-MAR-1994; 94US-0215087.  
 PR 14-APR-1994; 94US-0227369.  
 PR 01-JUN-1994; 94US-0251938.  
 PR 17-MAR-1995; 95WO-US03316.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.

XX  
 PI Kamb A;  
 XX  
 DR WPI: 1998-250421/22.  
 DR N-PSDB; AAV11238.  
 XX  
 PT DNA specific for Multiple Tumour Suppressor 161-beta gene - are  
 PT useful for the diagnosis of cancers related to MTS1E1-beta  
 PT mutation(s) and their treatment  
 XX  
 PS Disclosure: Column 63-64; 72pp; English.  
 XX  
 CC This sequence represents a human multiple tumour suppression protein,  
 CC MTS1. The MTS gene locus is also referred to as the familial melanoma  
 CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations  
 CC in MTS genes can be used in the diagnosis of predisposition to cancers,  
 CC e.g. melanoma, leukemia, astrocytoma, glioblastoma, lymphoma, glioma,  
 CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,  
 CC ovary, uterus, testis, kidney, stomach and rectum.  
 XX  
 SQ Sequence 156 AA:  
 Query Match 99.1%; Score 753; DB 19; Length 156;  
 Best Local Similarity 99.3%; Pred. No. 4.9e-82;  
 Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MESPADWLATAAARGVEEVRALLLEAVLPNAPNSYGRPRIOVMGMSARVAETLLHGA 60  
 Db 9 mepsadwlataaargveevrallleagalpnapnsygrripqymmgssarvae1111hga 68  
 QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVRDAMGRLPVDLAELGHRDVAR 120  
 Db 69 epncadpatltrpvhdaaregfldtlvvlhragarldvrdawgrlpvdlaeelghrdvar 128  
 QY 121 YLRAAGTGRGSHARIDAEGPSDIPD 148  
 Db 129 ylrraagtgrgsharidaegpsdipd 156

Search completed: September 19, 2002, 17:23:40  
 Job time: 39 sec



GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: September 19, 2002, 17:23:02 ; Search time 12.99 Seconds  
(without alignments)  
278.290 Million cell updates/sec

Title: US-09-016-869b-35  
Perfect score: 760  
Sequence: 1 MEPSADWLTAAARGREVEV.....TRGSNHRIDAEGSPDIPD 148

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues  
number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	760	100.0	148	1 US-08-154-915-4	Sequence 4, Appl1
2	760	100.0	148	3 US-08-384-106A-16	Sequence 16, Appl1
3	760	100.0	148	3 US-08-384-106A-24	Sequence 24, Appl1
4	760	100.0	148	5 PCT-US93-09945-4	Sequence 4, Appl1
5	760	100.0	156	2 US-08-627-610-2	Sequence 2, Appl1
6	760	100.0	156	2 US-08-306-511A-2	Sequence 2, Appl1
7	760	100.0	156	2 US-08-893-214-2	Sequence 2, Appl1
8	760	100.0	156	2 US-08-581-918A-2	Sequence 2, Appl1
9	760	100.0	156	4 US-08-346-147B-2	Sequence 2, Appl1
10	760	100.0	156	4 US-08-822-936-2	Sequence 2, Appl1
11	760	100.0	156	5 PCT-US95-04636-2	Sequence 2, Appl1
12	760	100.0	391	1 US-08-589-981-2	Sequence 2, Appl1
13	753	99.1	156	1 US-08-474-177-2	Sequence 2, Appl1
14	753	99.1	156	1 US-08-487-033-2	Sequence 2, Appl1
15	753	99.1	156	1 US-08-480-810-2	Sequence 2, Appl1
16	753	99.1	156	2 US-08-508-735-2	Sequence 2, Appl1
17	753	99.1	156	2 US-08-848-251-2	Sequence 2, Appl1
18	753	99.1	156	2 US-08-486-047-2	Sequence 2, Appl1
19	753	99.1	156	3 US-09-120-130-2	Sequence 2, Appl1
20	753	99.1	156	3 US-09-115-252-2	Sequence 2, Appl1
21	753	99.1	156	3 US-08-986-515-2	Sequence 2, Appl1
22	753	99.1	156	4 US-09-120-128-2	Sequence 2, Appl1
23	753	99.1	156	4 US-09-120-129-2	Sequence 2, Appl1
24	753	99.1	156	4 US-09-201-139-2	Sequence 2, Appl1
25	753	99.1	156	4 US-09-120-131-2	Sequence 2, Appl1
26	753	99.1	156	4 US-08-910-722-2	Sequence 2, Appl1
27	749.5	98.6	157	5 PCT-US96-05252-5	Sequence 5, Appl1

28	627.5	82.6	157	3 US-08-581-918A-12	Sequence 12, Appl1
29	627.5	82.6	157	4 US-08-346-147B-12	Sequence 12, Appl1
30	544	71.6	105	1 US-08-474-177-14	Sequence 14, Appl1
31	544	71.6	105	1 US-08-487-033-14	Sequence 14, Appl1
32	544	71.6	105	1 US-08-480-810-14	Sequence 14, Appl1
33	544	71.6	105	2 US-08-508-735-14	Sequence 14, Appl1
34	544	71.6	105	2 US-08-848-251-14	Sequence 14, Appl1
35	544	71.6	105	2 US-08-486-047-14	Sequence 14, Appl1
36	544	71.6	105	3 US-09-120-130-14	Sequence 14, Appl1
37	544	71.6	105	3 US-09-115-252-14	Sequence 14, Appl1
38	544	71.6	105	3 US-08-986-515-14	Sequence 14, Appl1
39	544	71.6	105	4 US-09-120-128-14	Sequence 14, Appl1
40	544	71.6	105	4 US-09-201-139-14	Sequence 14, Appl1
41	544	71.6	105	4 US-09-120-131-14	Sequence 14, Appl1
42	544	71.6	105	4 US-08-627-610-8	Sequence 8, Appl1
43	533	70.1	130	2 US-08-581-918A-8	Sequence 8, Appl1
44	533	70.1	130	3 US-08-346-147B-8	Sequence 8, Appl1
45	533	70.1	130	4 US-08-346-147B-8	Sequence 8, Appl1

## ALIGNMENTS

RESULT 1  
US-08-154-915-4  
; Sequence 4, Application US/08154915  
; Patent No. 5618669  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David  
; APPLICANT: Xiong, Yue  
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses  
; NUMBER OF INVENTION: Related Thereto  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/154,915  
; FILING DATE: 19-NOV-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/963,308  
; FILING DATE: 16-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/888,178  
; FILING DATE: 26-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/701,514  
; FILING DATE: 16-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 148 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-154-915-4

Query Match 100.0%; Score 760; DB 1; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.6e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLLHGA 60

DB 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLLHGA 60

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

DB 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

QY 121 YLRAAAGGTGSGNHARIDAEGSPDIP 148

DB 121 YLRAAAGGTGSGNHARIDAEGSPDIP 148

RESULT 2

US-08-384-106A-16  
Sequence 16, Application US/08384106A  
Patent No. 6033847

GENERAL INFORMATION:

APPLICANT: Sheer Ph.D., Charles J.

APPLICANT: Downing M.D., James

APPLICANT: Hirai Ph.D., Hiroshi

APPLICANT: Okuda, Tsukasa

TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/384,106A

FILING DATE: 06-FEB-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fox, Samuel L.

REGISTRATION NUMBER: 30,353

REFERENCE/DOCKET NUMBER: 0656, 0500000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 148 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-384-106A-16

Query Match 100.0%; Score 760; DB 3; Length 148;

Best Local Similarity 100.0%; Pred. No. 1.6e-83;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLLHGA 60

DB 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLLHGA 60

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

DB 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

QY 121 YLRAAAGGTGSGNHARIDAEGSPDIP 148

DB 121 YLRAAAGGTGSGNHARIDAEGSPDIP 148

RESULT 3

US-08-384-106A-24  
Sequence 24, Application US/08384106A  
Patent No. 6033847

GENERAL INFORMATION:

APPLICANT: Sheer Ph.D., Charles J.

APPLICANT: Downing M.D., James

APPLICANT: Hirai Ph.D., Hiroshi

APPLICANT: Okuda, Tsukasa

TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/384,106A

FILING DATE: 06-FEB-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fox, Samuel L.

REGISTRATION NUMBER: 30,353

REFERENCE/DOCKET NUMBER: 0656, 0500000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 148 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-384-106A-24

Query Match 100.0%; Score 760; DB 3; Length 148;

Best Local Similarity 100.0%; Pred. No. 1.6e-83;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLLHGA 60

DB 1 MEPSADWLATAARGVEEYRALLEVALPNAENSYGRPIQVMMGSAVAELLLHGA 60

QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

DB 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDMGRLPYDLAEELGHRDVAR 120

QY 121 YLRAAAGGTGSGNHARIDAEGSPDIP 148

DB 121 YLRAAAGGTGSGNHARIDAEGSPDIP 148

RESULT 4



PCT-US93-09945-4  
Sequence 4, Application PC/TUS9309945  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related  
TITLE OF INVENTION: Theteto  
NUMBER OF SEQUENCES: 4  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/09945  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/963,308  
FILING DATE: 16-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DEC-1992  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 148 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US93-09945-4

Query Match 100.0%; Score 760; DB 5; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.6e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEERALLLEAVALPNAFNSYGRPIQVMMGSAFYAEILLHGA 60  
DB 1 MEPSADWLATAAARGVEERALLLEAVALPNAFNSYGRPIQVMMGSAFYAEILLHGA 60

QY 61 EPNCADPATLTTPYHDARREGFLDTLVVLRHAGARLDVDRMGRLPVDLAEEIGHRDVAR 120  
DB 61 EPNCADPATLTTPYHDARREGFLDTLVVLRHAGARLDVDRMGRLPVDLAEEIGHRDVAR 120

QY 121 YLRAAAGTGRGSHARIDAEGPSDIPD 148  
DB 121 YLRAAAGTGRGSHARIDAEGPSDIPD 148

RESULT 5  
-627-610-2  
Sequence 2, Application US/08627610  
Patent No. 5919997  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Serrano, Manuel  
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle  
TITLE OF INVENTION: Regulation  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/627,610  
FILING DATE: 04-APR-1996

CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: CSI-001CP6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-627-610-2

Query Match 100.0%; Score 760; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.7e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEERALLLEAVALPNAFNSYGRPIQVMMGSAFYAEILLHGA 60  
DB 9 MEPSADWLATAAARGVEERALLLEAVALPNAFNSYGRPIQVMMGSAFYAEILLHGA 68

QY 61 EPNCADPATLTTPYHDARREGFLDTLVVLRHAGARLDVDRMGRLPVDLAEEIGHRDVAR 120  
DB 69 EPNCADPATLTTPYHDARREGFLDTLVVLRHAGARLDVDRMGRLPVDLAEEIGHRDVAR 128

QY 121 YLRAAAGTGRGSHARIDAEGPSDIPD 148  
DB 129 YLRAAAGTGRGSHARIDAEGPSDIPD 156

RESULT 6  
US-08-306-511A-2  
Sequence 2, Application US/08306511A  
Patent No. 5962316  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
TITLE OF INVENTION: Related Theteto  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,511A  
FILING DATE: 14-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: CSI-001CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-306-511A-2

Query Match 100.0%; Score 760; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.7e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALLLEAVLNPAPNSYGRPIQVMMGSAVAEILLHGA 60  
Db 9 MEPSADWLATAAARGVEEVRALLLEAVLNPAPNSYGRPIQVMMGSAVAEILLHGA 68

QY 61 EPNCADPATLTRPVHDAAREGFDTLVYLHRAGARLDVDMGRLPVDLAEEIGHRDVAR 120  
Db 69 EPNCADPATLTRPVHDAAREGFDTLVYLHRAGARLDVDMGRLPVDLAEEIGHRDVAR 128

QY 121 YLRAAGGTGSGNHARIDAAEGPSDIPD 148  
Db 129 YLRAAGGTGSGNHARIDAAEGPSDIPD 156

RESULT 7  
US-08-893-274-2  
Sequence 2, Application US/08893274  
Patent No. 5968821  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELLIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,274  
FILING DATE: 15-JULY-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEPTEMBER-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APRIL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOVEMBER-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DECEMBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/963,308  
FILING DATE: 16-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-071.09  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1000

TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-893-274-2

Query Match 100.0%; Score 760; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.7e-83;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADWLATAAARGVEEVRALLLEAVLNPAPNSYGRPIQVMMGSAVAEILLHGA 60  
Db 9 MEPSADWLATAAARGVEEVRALLLEAVLNPAPNSYGRPIQVMMGSAVAEILLHGA 68

QY 61 EPNCADPATLTRPVHDAAREGFDTLVYLHRAGARLDVDMGRLPVDLAEEIGHRDVAR 120  
Db 69 EPNCADPATLTRPVHDAAREGFDTLVYLHRAGARLDVDMGRLPVDLAEEIGHRDVAR 128

QY 121 YLRAAGGTGSGNHARIDAAEGPSDIPD 148  
Db 129 YLRAAGGTGSGNHARIDAAEGPSDIPD 156

RESULT 8  
US-08-581-918A-2  
Sequence 2, Application US/08581918A  
Patent No. 6043030  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Elliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordpad  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/581,918A  
FILING DATE: 02-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/497,214  
FILING DATE: 30-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/346,147  
FILING DATE: 29-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOV-1993



RESULT 13  
US-08-474-177-2  
; Sequence 2, Application US/08474177  
; Patent No. 5624819

GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-177-2

Query Match 99.1%; Score 753; DB 1; Length 156;  
Best Local Similarity 99.3%; Pred. No. 1.2e-82;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADMLATAAARGVEVRALLEVALPNAANSYGRPIQVMMGSAARVAEILLHGA 60  
DB 9 MEPSADMLATAAARGVEVRALLEVALPNAANSYGRPIQVMMGSAARVAEILLHGA 68  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDRAMGRLPVDLAEEELGHRDVAR 120  
DB 69 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDRAMGRLPVDLAEEELGHRDVAR 128  
QY 121 YLRAAAGTSGSNHARIDAEGPSDIPD 148  
DB 129 YLRAAAGTSGSNHARIDAEGPSDIPD 156

RESULT 14  
US-08-487-033-2  
Sequence 2, Application US/08487033  
Patent No. 5739027  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1-Beta GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,033  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-033-2

Query Match 99.1%; Score 753; DB 1; Length 156;  
Best Local Similarity 99.3%; Pred. No. 1.2e-82;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSADMLATAAARGVEVRALLEVALPNAANSYGRPIQVMMGSAARVAEILLHGA 60  
DB 9 MEPSADMLATAAARGVEVRALLEVALPNAANSYGRPIQVMMGSAARVAEILLHGA 68  
QY 61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDRAMGRLPVDLAEEELGHRDVAR 120  
DB 69 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDRAMGRLPVDLAEEELGHRDVAR 128  
QY 121 YLRAAAGTSGSNHARIDAEGPSDIPD 148  
DB 129 YLRAAAGTSGSNHARIDAEGPSDIPD 156

## RESULT 15

US-08-480-810-2

; Sequence 2, Application US/08480810

; Patent No. 5801236

; GENERAL INFORMATION:

; APPLICANT: Kamb, Alexander

; TITLE OF INVENTION: MTS1 GENE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Venable, Baetjer, Howard &amp; Civiletti, LLP

; STREET: 1201 New York Avenue, Suite 1000

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/480,810

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/03316

; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/251,938

; FILING DATE: 01-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,087

; FILING DATE: 18-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,086

; FILING DATE: 18-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/214,582

; FILING DATE: 18-MAR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Innen, Jeffrey L.

; REGISTRATION NUMBER: 28,957

; REFERENCE/DOCKET NUMBER: 24884-109348

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-962-4810

; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 156 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-480-810-2

Query Match 99.1%; Score 753; DB 1; Length 156;  
Best Local Similarity 99.3%; Pred. No. 1.2e-82;  
Matches 147; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MEPSADWLATAAARGVEVRALLLEAVALLPNAPNSYGRPIQVMMGSAFYAEILLHGA 60  
DB 9 MEPSADWLATAAARGVEVRALLLEAGALPNAPNSYGRPIQVMMGSAFYAEILLHGA 68  
OY 61 EPNCADPRLTLRPVVDARREGFLDTLVVLRAGARLDVDRAMGRLPVDLAELGHRDVAR 120  
DB 69 EPNCADPRLTLRPVVDARREGFLDTLVVLRAGARLDVDRAMGRLPVDLAELGHRDVAR 128  
OY 121 YLRAAAGTGRGSHARIDAAEGSPDIPD 148

DB 129 YLRAAAGTGRGSHARIDAAEGSPDIPD 156

Search completed: September 19, 2002, 17:24:00  
Job time: 58 sec

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## OM protein - protein search, using sw model

Run on: September 19, 2002, 17:25:12 ; Search time 12.89 Seconds  
(without alignments)  
280.449 Million cell updates/sec

Title: US-09-016-869b-35  
Perfect score: 148  
Sequence: 1 MEPSADWLATAARGRVREV.....TRGSNHARIDAEGPSIDP 148

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Size: 0  
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	148	100.0	148	1 US-08-154-915-4	Sequence 4, Appl
2	148	100.0	148	3 US-08-384-106A-16	Sequence 16, Appl
3	148	100.0	148	3 US-08-384-106A-24	Sequence 24, Appl
4	148	100.0	148	5 PCT-US93-09945-4	Sequence 4, Appl
5	148	100.0	156	2 US-08-627-610-2	Sequence 2, Appl
6	148	100.0	156	2 US-08-306-511A-2	Sequence 2, Appl
7	148	100.0	156	2 US-08-893-274-2	Sequence 2, Appl
8	148	100.0	156	3 US-08-581-918A-2	Sequence 2, Appl
9	148	100.0	156	4 US-08-346-147B-2	Sequence 2, Appl
10	148	100.0	156	4 US-08-822-936-2	Sequence 2, Appl
11	148	100.0	156	5 PCT-US95-04636-2	Sequence 2, Appl
12	148	100.0	391	1 US-08-589-981-2	Sequence 2, Appl
13	148	100.0	156	1 US-08-474-177-2	Sequence 2, Appl
14	148	100.0	156	1 US-08-487-033-2	Sequence 2, Appl
15	148	100.0	156	1 US-08-480-810-2	Sequence 2, Appl
16	148	100.0	156	2 US-08-508-735-2	Sequence 2, Appl
17	148	100.0	156	2 US-08-848-251-2	Sequence 2, Appl
18	148	100.0	156	2 US-08-486-047-2	Sequence 2, Appl
19	148	100.0	156	3 US-09-120-130-2	Sequence 2, Appl
20	148	100.0	156	3 US-09-115-252-2	Sequence 2, Appl
21	148	100.0	156	3 US-08-986-515-2	Sequence 2, Appl
22	148	100.0	156	4 US-09-120-128-2	Sequence 2, Appl
23	148	100.0	156	4 US-09-120-129-2	Sequence 2, Appl
24	148	100.0	156	4 US-09-201-139-2	Sequence 2, Appl
25	148	100.0	156	4 US-09-120-131-2	Sequence 2, Appl
26	148	100.0	156	4 US-08-910-722-2	Sequence 2, Appl
27	148	100.0	105	1 US-08-474-177-14	Sequence 14, Appl

28	105	70.9	105	1 US-08-487-033-14	Sequence 14, Appl
29	105	70.9	105	1 US-08-480-810-14	Sequence 14, Appl
30	105	70.9	105	2 US-08-508-735-14	Sequence 14, Appl
31	105	70.9	105	2 US-08-848-251-14	Sequence 14, Appl
32	105	70.9	105	2 US-08-486-047-14	Sequence 14, Appl
33	105	70.9	105	3 US-09-120-130-14	Sequence 14, Appl
34	105	70.9	105	3 US-09-115-252-14	Sequence 14, Appl
35	105	70.9	105	3 US-08-986-515-14	Sequence 14, Appl
36	105	70.9	105	4 US-09-120-128-14	Sequence 14, Appl
37	105	70.9	105	4 US-09-120-129-14	Sequence 14, Appl
38	105	70.9	105	4 US-09-201-139-14	Sequence 14, Appl
39	105	70.9	105	4 US-09-120-131-14	Sequence 14, Appl
40	95	64.2	157	5 PCT-US96-05252-5	Sequence 5, Appl
41	89	60.1	89	3 US-08-581-918A-37	Sequence 37, Appl
42	89	60.1	89	4 US-08-346-147B-37	Sequence 37, Appl
43	72	48.6	88	3 US-08-581-918A-38	Sequence 38, Appl
44	72	48.6	88	4 US-08-346-147B-38	Sequence 38, Appl
45	72	48.6	136	5 PCT-US96-05252-6	Sequence 6, Appl
46	72	48.6	137	5 US-08-306-511A-4	Sequence 4, Appl
47	72	48.6	137	2 US-08-893-274-4	Sequence 4, Appl
48	72	48.6	138	1 US-08-474-177-16	Sequence 16, Appl
49	72	48.6	138	1 US-08-487-033-16	Sequence 16, Appl
50	72	48.6	138	1 US-08-480-810-16	Sequence 16, Appl
51	72	48.6	138	2 US-08-508-735-16	Sequence 16, Appl
52	72	48.6	138	2 US-08-627-610-4	Sequence 4, Appl
53	72	48.6	138	2 US-08-848-251-16	Sequence 16, Appl
54	72	48.6	138	2 US-08-486-047-16	Sequence 16, Appl
55	72	48.6	138	3 US-08-384-106A-25	Sequence 25, Appl
56	72	48.6	138	3 US-09-120-130-16	Sequence 16, Appl
57	72	48.6	138	3 US-08-581-918A-4	Sequence 16, Appl
58	72	48.6	138	3 US-09-115-252-16	Sequence 16, Appl
59	72	48.6	138	3 US-08-986-515-16	Sequence 16, Appl
60	72	48.6	138	4 US-09-120-128-16	Sequence 16, Appl
61	72	48.6	138	4 US-09-120-129-16	Sequence 16, Appl
62	72	48.6	138	4 US-09-201-139-16	Sequence 16, Appl
63	72	48.6	138	4 US-08-346-147B-4	Sequence 4, Appl
64	72	48.6	138	4 US-09-120-131-16	Sequence 16, Appl
65	72	48.6	138	4 US-08-822-936-4	Sequence 4, Appl
66	72	48.6	138	5 PCT-US95-04636-4	Sequence 4, Appl
67	62	41.9	77	2 US-08-893-274-8	Sequence 8, Appl
68	62	41.9	77	2 US-08-306-511A-8	Sequence 8, Appl
69	62	41.9	130	2 US-08-627-610-8	Sequence 8, Appl
70	62	41.9	130	3 US-08-581-918A-8	Sequence 8, Appl
71	62	41.9	130	4 US-08-346-147B-8	Sequence 8, Appl
72	62	41.9	130	4 US-08-822-936-8	Sequence 8, Appl
73	62	41.9	130	5 PCT-US95-04636-8	Sequence 8, Appl
74	52	35.1	52	1 US-08-249-371-2	Sequence 2, Appl
75	52	35.1	52	5 PCT-US95-06451-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-154-915-4  
; Sequence 4, Application US/08154915  
; Patent No. 5618669  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David  
; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/154, 915
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991, 997
; FILING DATE: 17-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963, 308
; FILING DATE: 16-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888, 178
; FILING DATE: 26-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701, 514
; FILING DATE: 16-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIT-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-154-915-4

Query Match          100.0%; Score 148; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 1,4e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSADWLTAARGVEEVALLEAVLPPNAPNSYGRRIQVMMGSAVAELLHLGA 60
DB 1 MESSADWLTAARGVEEVALLEAVLPPNAPNSYGRRIQVMMGSAVAELLHLGA 60
QY 61 EPNCADPATLTRPVHDAREGEFLDTLVYLHRAGARLDVDPAMGRLPVDLAEEIGHRDVAR 120
DB 61 EPNCADPATLTRPVHDAREGEFLDTLVYLHRAGARLDVDPAMGRLPVDLAEEIGHRDVAR 120
QY 121 YLRAAGGTGSGNHARIDAEGPSDIPD 148
DB 121 YLRAAGGTGSGNHARIDAEGPSDIPD 148
QY 121 YLRAAGGTGSGNHARIDAEGPSDIPD 148
DB 121 YLRAAGGTGSGNHARIDAEGPSDIPD 148

RESULT 2
US-08-384-106A-16
; Sequence 16, Application US/08384106A
; Patent No. 6033847
; GENERAL INFORMATION:
; APPLICANT: Sherr Ph.D., Charles J.
; APPLICANT: Downing M.D., James
; APPLICANT: Hirai Ph.D., Hiroshi
; APPLICANT: Okuda, Tsukasa
; TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of
; CYCLIN DEPENDENT KINASES CDK4 AND CDK6, AND USES THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,106A
; FILING DATE: 06-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0500000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-384-106A-16

Query Match          100.0%; Score 148; DB 3; Length 148;
Best Local Similarity 100.0%; Pred. No. 1,4e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSADWLTAARGVEEVALLEAVLPPNAPNSYGRRIQVMMGSAVAELLHLGA 60
DB 1 MESSADWLTAARGVEEVALLEAVLPPNAPNSYGRRIQVMMGSAVAELLHLGA 60
QY 61 EPNCADPATLTRPVHDAREGEFLDTLVYLHRAGARLDVDPAMGRLPVDLAEEIGHRDVAR 120
DB 61 EPNCADPATLTRPVHDAREGEFLDTLVYLHRAGARLDVDPAMGRLPVDLAEEIGHRDVAR 120
QY 121 YLRAAGGTGSGNHARIDAEGPSDIPD 148
DB 121 YLRAAGGTGSGNHARIDAEGPSDIPD 148

RESULT 3
US-08-384-106A-24
; Sequence 24, Application US/08384106A
; Patent No. 6033847
; GENERAL INFORMATION:
; APPLICANT: Sherr Ph.D., Charles J.
; APPLICANT: Downing M.D., James
; APPLICANT: Hirai Ph.D., Hiroshi
; APPLICANT: Okuda, Tsukasa
; TITLE OF INVENTION: Ink4c-p18 and Ink4d-p19, Inhibitors of
; CYCLIN DEPENDENT KINASES CDK4 AND CDK6, AND USES THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,106A
; FILING DATE: 06-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0500000
; TELECOMMUNICATION INFORMATION:
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: TELEPHONE: 202-571-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 24:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 148 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: peptide
:
: OS-08-384-106a-24

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Query Match	100.0%;	Score 148;	DB 3;	Length 148;
Best Local Similarity	100.0%;	Pred. No. 1.4e-130;		
Matches 148; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Accession	Sequence	Length
Oy	1 MEPSADMTATAAGRGVEEVALLLEAAALPAAPSYSTRPTIQVMMGMSAVAEITLLHGA	60
Db	1 MEPSADMTATAAGRGVEEVALLLEAAALPAAPSYSTRPTIQVMMGMSAVAEITLLHGA	60
Oy	61 EPNCADPRTILRPVHDARREGFTLTLVYLRHAGARLDVPMAGSLPVDLAELGHRDVAR	120
Db	61 EPNCADPRTILRPVHDARREGFTLTLVYLRHAGARLDVPMAGSLPVDLAELGHRDVAR	120
Oy	121 YLRAAAGTGRGSHNARIDAEPSDIPD	148
Db	121 YLRAAAGTGRGSHNARIDAEPSDIPD	148

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1      RESULT          4
2      PCT-US93-09945-4
3      ; Sequence 4, Application PC/TUS9309945
4      ; GENERAL INFORMATION:
5      ; APPLICANT:
6      ; TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related
7      ; TITLE OF INVENTION: Therefo
8      ; NUMBER OF SEQUENCES: 4
9      ; COMPUTER READABLE FORM:
10     ; MEDIUM TYPE: Floppy disk
11     ; COMPUTER: IBM PC compatible
12     ; OPERATING SYSTEM: PC-DOS/MS-DOS
13     ; SOFTWARE: ASCII(text)
14     ; CURRENT APPLICATION DATA:
15     ; APPLICATION NUMBER: PCT/US93/09945
16     ; FILING DATE:
17     ; PRIOR APPLICATION DATA:
18     ; APPLICATION NUMBER: US 07/963,308
19     ; FILING DATE: 16-OCT-1992
20     ; PRIOR APPLICATION DATA:
21     ; APPLICATION NUMBER: US 07/991,997
22     ; FILING DATE: 17-DEC-1992
23     ; INFORMATION FOR SEQ ID NO: 4:
24     ; SEQUENCE CHARACTERISTICS:
25     ; LENGTH: 148 amino acids
26     ; type: amino acid
27     ; TOPOLOGY: linear
28     ; MOLECULE TYPE: protein
29     ; PCT-US93-09945-4

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Query Match	100.0%;	Score 148;	DB 5;	Length 148;
Best Local Similarity	100.0%;	Pred. No. 1.4e-130;		
Matches 148;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

Qy 1 MPPSADMLTAAABRRVEEVALLEAVALLPNAAPMSYGRPLQVMMMSARVAEELLILHGA 60  
Db 1 MPPSADMLTAAABRRVEEVALLEAVALLPNAAPMSYGRPLQVMMMSARVAEELLILHGA 60  
Qy 61 EPNCADPATLTLPVHDAAREGFLDTLVYLHRRGARDLYRDAMGSLPYDLAEELGHRVAR 120  
Db 61 EPNCADPATLTLPVHDAAREGFLDTLVYLHRRGARDLYRDAMGSLPYDLAEELGHRVAR 120  
Qy 121 YLRMAAGGTGRGNNHAKITDAEESPDI 148

Db 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148

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1  RESULT      5
2  US-08-627-610-2
3  ; Sequence 2, Application US/08627610
4  ; Patent No. 591997
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Beach, David H.
7  ; APPLICANT: Serrano, Manuel
8  ; APPLICANT: Delipho, Ronald A.
9  ; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
10 ; TITLE OF INVENTION: Regulation
11 ; NUMBER OF SEQUENCES: 13
12 ; CORRESPONDENCE ADDRESS:
13 ; ADDRESSEE: LAHIVE & COCKFIELD
14 ; STREET: 60 State Street
15 ; CITY: Boston
16 ; STATE: MA
17 ; COUNTRY: USA
18 ; ZIP: 02109
19 ; COMPUTER READABLE FORM:
20 ; MEDIUM TYPE: Floppy disk
21 ; COMPUTER: IBM PC compatible
22 ; OPERATING SYSTEM: PC-DOS/MS-DOS
23 ; SOFTWARE: ASCII(text)
24 ; CURRENT APPLICATION DATA:
25 ; APPLICATION NUMBER: US/08/627,610
26 ; FILING DATE: 04-APR-1996
27 ; CLASSIFICATION: 800
28 ; ATTORNEY/AGENT INFORMATION:
29 ; NAME: Vincent, Matthew P.
30 ; REGISTRATION NUMBER: 36,709
31 ; REFERENCE/DOCKET NUMBER: CSI-001CP6
32 ; TELECOMMUNICATION INFORMATION:
33 ; TELEPHONE: (617) 227-7400
34 ; TELEFAX: (617) 227-5941
35 ; INFORMATION FOR SEQ ID NO: 2:
36 ; SEQUENCE CHARACTERISTICS:
37 ; LENGTH: 156 amino acids
38 ; TYPE: amino acid
39 ; TOPOLOGY: linear
40 ; MOLECULE TYPE: protein
41 ;
42 US-08-627-610-2

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Query Match	100.0%	Score 148:	DB 2;	Length 156;
Best local Similarity	100.0%	Pred.	No. 1.5e130;	
Matches 148; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY 1 MESSAWMLTAAARGVEEVRALLAEVALPNAPNSYGRPIQVMMGSGARVAELLTLHGA 60

Db 9 MESSAWMLTAAARGVEEVRALLAEVALPNAPNSYGRPIQVMMGSGARVAELLTLHGA 68

QY 61 EPNCAPDALTTPYNDAAEEGPLTVLVLHARGALDYRDAMGRLPYDLAEELGHRDYAR 120

Db 69 EPNCAPDALTTPYNDAAEEGPLTVLVLHARGALDYRDAMGRLPYDLAEELGHRDYAR 128

QY 121 YLRAAAGTGRGSNHARIDAEGSPDIPD 148

Db 129 YLRAAAGTGRGSNHARIDAEGSPDIPD 156

RESULT 6  
US-08-306-511A-2  
Sequence 2, Application US/08306511A  
Patent No 5963316  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.

```

; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-306-511A-2

Query Match      100.0%; Score 148; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MEPSADWLATAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAELLHLHGA 60
        |||||||
DB      9 MEPSADWLATAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAELLHLHGA 68
QY      61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDMGRLPVDLAELGHRDVAR 120
        |||||||
DB      69 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDMGRLPVDLAELGHRDVAR 128
QY      121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148
        |||||||
        129 YLRAAAGGTRGSNHARIDAEGPSDIPD 156

RESULT      7
; US-08-893-274-2
; Sequence 2, Application US/08893274
; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,274
; FILING DATE: 15-JULY-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APRIL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOVEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DECEMBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-893-274-2

Query Match      100.0%; Score 148; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MEPSADWLATAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAELLHLHGA 60
        |||||||
DB      9 MEPSADWLATAARGVEEVRALLLEAVLPNAPNSYGRPIQVMMGSAVAELLHLHGA 68
QY      61 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDMGRLPVDLAELGHRDVAR 120
        |||||||
DB      69 EPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVDMGRLPVDLAELGHRDVAR 128
QY      121 YLRAAAGGTRGSNHARIDAEGPSDIPD 148
        |||||||
        129 YLRAAAGGTRGSNHARIDAEGPSDIPD 156

RESULT      8
; US-08-581-918A-2
; Sequence 2, Application US/08581918A
; Patent No. 6043030
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELLIOT
; STREET: One Post Office Square
; CITY: Boston
```

```
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-581-918A-2

Query Match          100.0%; Score 148; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,147B
FILING DATE: 29-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.04
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-346-147B-2

Query Match          100.0%; Score 148; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-130;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 391 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-589-981-2

Query Match 100.0%; Score 148; DB 1; Length 391;  
Best Local Similarity 100.0%; Pred. No. 3.5e-130;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPADWATATAGRGVEEVALLLEAVALPAPNSYGRPIQVMMGSARVAELLHGA 60  
DB 244 MEPADWATATAGRGVEEVALLLEAVALPAPNSYGRPIQVMMGSARVAELLHGA 303  
QY 61 EPNCADPATLTRPVHDAREGFLDTLVLRHAGARLDVPRAMGRLPVDLAEELGHRDVAR 120  
DB 304 EPNCADPATLTRPVHDAREGFLDTLVLRHAGARLDVPRAMGRLPVDLAEELGHRDVAR 363  
QY 121 YLRAAAGTGRGSHNRIDAAEGPSDIPD 148  
DB 364 YLRAAAGTGRGSHNRIDAAEGPSDIPD 391

RESULT 13  
US-08-474-177-2

Sequence 2, Application US/08474177  
Patent No. 5624819  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
TITLE OF INVENTION: GERM-LINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-177-2

Query Match 81.8%; Score 121; DB 1; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2.1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSARVAELLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSARVAELLHGAEPNCADPATLTRPVHDAREGFLDTLV 95  
QY 88 VLHAGARLDVPRAMGRLPVDLAEELGHRDVARYLRAAAGTGRGSHNRIDAAEGPSDIP 147  
DB 96 VLHAGARLDVPRAMGRLPVDLAEELGHRDVARYLRAAAGTGRGSHNRIDAAEGPSDIP 155  
QY 148 D 148  
DB 156 D 156

RESULT 14  
US-08-487-033-2

Sequence 2, Application US/08487033  
Patent No. 5739027  
GENERAL INFORMATION:  
APPLICANT: Ramb, Alexander  
TITLE OF INVENTION: MTS1E1-Beta GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,033  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957

NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-033-2

Query Match 81.8%; Score 121; DB 1; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2,1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

28 ALPNAPNSYGRPIQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
|||||  
36 ALPNAPNSYGRPIQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLV 95  
|||||  
QY 88 VLHRAGARLDVWDAGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPSDIP 147  
|||||  
DB 96 VLHRAGARLDVWDAGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPSDIP 155  
|||||  
QY 148 D 148  
DB 156 D 156

RESULT 15  
US-08-480-810-2  
Sequence 2, Application US/08480810  
Patent No. 5801236  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,810  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-480-810-2

Query Match 81.8%; Score 121; DB 1; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2,1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
|||||  
DB 36 ALPNAPNSYGRPIQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLV 95  
|||||  
QY 88 VLHRAGARLDVWDAGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPSDIP 147  
|||||  
DB 96 VLHRAGARLDVWDAGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPSDIP 155  
|||||  
QY 148 D 148  
DB 156 D 156

RESULT 16  
US-08-508-735-2  
Sequence 2, Application US/08508735  
Patent No. 5843756  
GENERAL INFORMATION:  
APPLICANT: Stone, Steven  
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/508,735  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: US to be assigned  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4848  
TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-508-735-2

Query Match 81.8%; Score 121; DB 2; Length 156;  
Best local similarity 100.0%; Pred. No. 2,1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSAVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95

QY 88 VLRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTGRSGNHARIDAAGSPDIP 147  
DB 96 VLRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTGRSGNHARIDAAGSPDIP 155

QY 148 D 148  
DB 156 D 156

RESULT 17  
US-08-848-251-2  
Sequence 2, Application US/0848251  
Patent No. 5989815  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND  
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS  
TITLE OF INVENTION: GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/848,251  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/474,083  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-848-251-2

Query Match 81.8%; Score 121; DB 2; Length 156;  
Best local similarity 100.0%; Pred. No. 2,1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSAVAEELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95

QY 88 VLRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTGRSGNHARIDAAGSPDIP 147  
DB 96 VLRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTGRSGNHARIDAAGSPDIP 155

QY 148 D 148  
DB 156 D 156

RESULT 18  
US-08-486-047-2  
Sequence 2, Application US/08486047  
Patent No. 5994095  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS2 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,047  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994

```

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/214,582
: FILING DATE: 18-MAR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Innen, Jeffrey L.
: REGISTRATION NUMBER: 28,957
: REFERENCE/DOCKET NUMBER: 24884-109348-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-962-4810
: TELEFAX: 202-962-8300
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 156 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-486-047-2

Query Match      81.8%; Score 121; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAKVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
DB 36 ALPNAPNSYGRPIQVMMGSAKVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95
QY 88 VLHRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147
DB 96 VLHRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 155
QY 148 D 148
DB 156 D 156

RESULT 19
US-09-120-130-2
: Sequence 2, Application US/09120130
: Patent No. 6037462
: GENERAL INFORMATION:
: APPLICANT: Kamb, Alexander
: TITLE OF INVENTION: MTS1 GENE
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
: STREET: 1201 New York Avenue, Suite 1000
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/120,130
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/480,810
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/251,938
: FILING DATE: 01-JUN-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/215,087
: FILING DATE: 18-MAR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/215,086
: FILING DATE: 18-MAR-1994
: PRIOR APPLICATION DATA:
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: APPLICATION NUMBER: US 08/227,369
: FILING DATE: 14-APR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/214,582
: FILING DATE: 18-MAR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Innen, Jeffrey L.
: REGISTRATION NUMBER: 28,957
: REFERENCE/DOCKET NUMBER: 24884-109348
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-962-4810
: TELEFAX: 202-962-8300
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 156 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-120-130-2

Query Match      81.8%; Score 121; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAKVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
DB 36 ALPNAPNSYGRPIQVMMGSAKVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95
QY 88 VLHRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147
DB 96 VLHRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 155
QY 148 D 148
DB 156 D 156

RESULT 20
US-09-115-252-2
: Sequence 2, Application US/09115252
: Patent No. 6060301
: GENERAL INFORMATION:
: APPLICANT: Kamb, Alexander
: TITLE OF INVENTION: MTS1 GENE
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
: STREET: 1201 New York Avenue, Suite 1000
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/115,252
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/480,810
: FILING DATE: 07-JUN-1995
: APPLICATION NUMBER: PCT/US95/03316
: FILING DATE: 17-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/251,938
: FILING DATE: 01-JUN-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/215,087
: FILING DATE: 18-MAR-1994
```



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-115-252-2

Query Match 81.8%; Score 121; DB 3; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2,1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRRIQVMMGSAFVAELLHLHGAEPCADPATLTTRPVHDAAREGFDTLV 87  
DB 36 ALPNAPNSYGRRIQVMMGSAFVAELLHLHGAEPCADPATLTTRPVHDAAREGFDTLV 95  
QY 88 VLRAGARLDVDRAMGRPLVDLAELGHRDVARYTLRAAAGTSGSNHARIDAEGPSDIP 147  
DB 96 VLRAGARLDVDRAMGRPLVDLAELGHRDVARYTLRAAAGTSGSNHARIDAEGPSDIP 155  
QY 148 D 148  
DB 156 D 156

RESULT 21  
US-08-986-515-2  
Sequence 2, Application US/08986515  
Patent No. 6090578  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/986,515  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/480,810  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-986-515-2

Query Match 81.8%; Score 121; DB 3; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2,1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRRIQVMMGSAFVAELLHLHGAEPCADPATLTTRPVHDAAREGFDTLV 87  
DB 36 ALPNAPNSYGRRIQVMMGSAFVAELLHLHGAEPCADPATLTTRPVHDAAREGFDTLV 95  
QY 88 VLRAGARLDVDRAMGRPLVDLAELGHRDVARYTLRAAAGTSGSNHARIDAEGPSDIP 147  
DB 96 VLRAGARLDVDRAMGRPLVDLAELGHRDVARYTLRAAAGTSGSNHARIDAEGPSDIP 155  
QY 148 D 148  
DB 156 D 156

RESULT 22  
US-09-120-128-2  
Sequence 2, Application US/09120128  
Patent No. 6140473  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS2 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120,128  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,047  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-4810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-120-128-2

Query Match      81.8%; Score 121; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
DB 36 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95
QY 88 VLHRAGARLDVNDAMGRPLVLDLAELGHRDVARYLRAAAGSTRGSNHARIDAAEGPSDIP 147
DB 96 VLHRAGARLDVNDAMGRPLVLDLAELGHRDVARYLRAAAGSTRGSNHARIDAAEGPSDIP 155
QY 148 D 148
DB 156 D 156

LT 23
9-120-129-2
; Sequence 2, Application US/09120129
; Patent No. 6180776
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,129
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/486,047
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-120-129-2

Query Match      81.8%; Score 121; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87
DB 36 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95
QY 88 VLHRAGARLDVNDAMGRPLVLDLAELGHRDVARYLRAAAGSTRGSNHARIDAAEGPSDIP 147
DB 96 VLHRAGARLDVNDAMGRPLVLDLAELGHRDVARYLRAAAGSTRGSNHARIDAAEGPSDIP 155
QY 148 D 148
DB 156 D 156

RESULT 24
US-09-201-139-2
; Sequence 2, Application US/09201139
; Patent No. 6210949
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/201,139  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/508,735  
FILING DATE:  
PRIOR APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4848  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-201-139-2

Query Match 81.8%; Score 121; DB 4; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2.1e-105; Mismatches 0; Indels 0; Gaps 0;  
Matches 121; Conservative 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPCADPATLTRPVHDAAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPCADPATLTRPVHDAAREGFLDTLV 95  
QY 88 VLRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIP 147  
DB 96 VLRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIP 155  
QY 148 D 148  
DB 156 D 156

RESULT 25  
US-09-120-131-2  
Sequence 2, Application US/09120131  
Patent No. 6218146  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS2 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120,131  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,047  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-120-131-2

Query Match 81.8%; Score 121; DB 4; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2.1e-105; Mismatches 0; Indels 0; Gaps 0;  
Matches 121; Conservative 0;

QY 28 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPCADPATLTRPVHDAAREGFLDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSAVAELLHLHGAEPCADPATLTRPVHDAAREGFLDTLV 95  
QY 88 VLRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIP 147  
DB 96 VLRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIP 155  
QY 148 D 148  
DB 156 D 156

RESULT 26  
US-08-910-722-2  
Sequence 2, Application US/08910722  
Patent No. 6251871  
GENERAL INFORMATION:  
APPLICANT: Jiro, Xiaomei  
TITLE OF INVENTION: P16 EXPRESSION CONSTRUCTS AND THEIR  
TITLE OF INVENTION: APPLICATION IN CANCER THERAPY  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,722  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/502,881  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hignlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: INGN:016/HYL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 156 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
08-910-722-2

Query Match 81.8%; Score 121; DB 4; Length 156;  
Best Local Similarity 100.0%; Pred. No. 2,1e-105;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAFYAEILLHGAEPCADPATLTRPVHDAREGFELDTLV 87  
DB 36 ALPNAPNSYGRPIQVMMGSAFYAEILLHGAEPCADPATLTRPVHDAREGFELDTLV 95  
QY 88 VLHRAGARLDVDRAMGRLPVDLAELGHRDVARYLRAAAGSTRGSHNARIDAEGPSDIP 147  
DB 96 VLHRAGARLDVDRAMGRLPVDLAELGHRDVARYLRAAAGSTRGSHNARIDAEGPSDIP 155

QY 148 D 148  
DB 156 D 156

RESULT 27  
US-08-474-177-14  
Sequence 14, Application US/08474177  
Patent No. 5624819  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-177-14

Query Match 70.9%; Score 105; DB 1; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1,1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSAFYAEILLHGAEPCADPATLTRPVHDAREGFELDTLVVLHRAGARLDVDRAMG 103  
DB 1 MMGSAFYAEILLHGAEPCADPATLTRPVHDAREGFELDTLVVLHRAGARLDVDRAMG 60  
QY 104 RLPVDLAELGHRDVARYLRAAAGSTRGSHNARIDAEGPSDIP 148  
DB 61 RLPVDLAELGHRDVARYLRAAAGSTRGSHNARIDAEGPSDIP 105

RESULT 28  
US-08-487-033-14  
Sequence 14, Application US/08487033  
Patent No. 5739027  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1-Beta GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,033  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-487-033-14

Query Match 70.9%; Score 105; DB 1: Length 105;  
Best Local Similarity 100.0%; Pred. No. 1,1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVAEELLHGAEPCADPATLTRPVHDAREGFDTLVVLRAGARLDVVDAMG 103  
|||||  
DB 1 MMGSARVAEELLHGAEPCADPATLTRPVHDAREGFDTLVVLRAGARLDVVDAMG 60  
|||||  
QY 104 RLPVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAEGPSDIPD 148  
|||||  
DB 61 RLPVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAEGPSDIPD 105  
|||||

RESULT 29  
US-08-480-810-14  
Sequence 14, Application US/08480810  
Patent No. 5801236  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,810  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-480-810-14

Query Match 70.9%; Score 105; DB 1: Length 105;  
Best Local Similarity 100.0%; Pred. No. 1,1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVAEELLHGAEPCADPATLTRPVHDAREGFDTLVVLRAGARLDVVDAMG 103  
|||||  
DB 1 MMGSARVAEELLHGAEPCADPATLTRPVHDAREGFDTLVVLRAGARLDVVDAMG 60  
|||||  
QY 104 RLPVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAEGPSDIPD 148  
|||||  
DB 61 RLPVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAEGPSDIPD 105  
|||||

RESULT 30  
US-08-508-735-14  
Sequence 14, Application US/08508735  
Patent No. 5843756  
GENERAL INFORMATION:  
APPLICANT: Stone, Steven  
APPLICANT: Jiang, Ping  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/508,735  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US to be assigned  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4848

TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-508-735-14

Query Match 70.9%; Score 105; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSAVAVELLHLHGAEPCADPATLTTPVHDAREGFDTLVYLHRAGARLDVRDAMG 103  
DB 1 MMGSAVAVELLHLHGAEPCADPATLTTPVHDAREGFDTLVYLHRAGARLDVRDAMG 60  
QY 104 RLVPDLAEELGHRDVARYLRAAAGTGRGSHNARIIDAEGPSDIPD 148  
61 RLVPDLAEELGHRDVARYLRAAAGTGRGSHNARIIDAEGPSDIPD 105

RESULT 31  
US-08-848-251-14  
Sequence 14, Application US/08848251  
Patent No. 5989815  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon Albricht, Lisa A.  
TITLE OF INVENTION: GEMLINE MUTATIONS IN THE MTS GENE AND  
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS  
TITLE OF INVENTION: GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/848,251  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/474,083  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-848-251-14

Query Match 70.9%; Score 105; DB 2; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSAVAVELLHLHGAEPCADPATLTTPVHDAREGFDTLVYLHRAGARLDVRDAMG 103  
DB 1 MMGSAVAVELLHLHGAEPCADPATLTTPVHDAREGFDTLVYLHRAGARLDVRDAMG 60  
QY 104 RLVPDLAEELGHRDVARYLRAAAGTGRGSHNARIIDAEGPSDIPD 148  
DB 61 RLVPDLAEELGHRDVARYLRAAAGTGRGSHNARIIDAEGPSDIPD 105

RESULT 32  
US-08-486-047-14  
Sequence 14, Application US/08486047  
Patent No. 5994095  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS2 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,047  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-486-047-14

Query Match  
Best Local Similarity 70.9%; Score 105; DB 2; Length 105;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVALLLHGAEPCADPATLTTPVHDAREGFLDTLVVLRAGARLDVWDAMG 103  
|||||  
DB 1 MMGSARVALLLHGAEPCADPATLTTPVHDAREGFLDTLVVLRAGARLDVWDAMG 60  
|||||

QY 104 RLPVDLAEELGHRDVARYLRAAAGTSGSNHARIDAAEGSPDIPD 148  
|||||  
DB 61 RLPVDLAEELGHRDVARYLRAAAGTSGSNHARIDAAEGSPDIPD 105  
|||||

RESULT 33  
US-09-120-130-14  
Sequence 14, Application US/09120130  
Patent No. 6037462  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120.130  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/480, 810  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-120-130-14

Query Match  
Best Local Similarity 70.9%; Score 105; DB 3; Length 105;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVALLLHGAEPCADPATLTTPVHDAREGFLDTLVVLRAGARLDVWDAMG 103  
|||||  
DB 1 MMGSARVALLLHGAEPCADPATLTTPVHDAREGFLDTLVVLRAGARLDVWDAMG 60  
|||||

QY 104 RLPVDLAEELGHRDVARYLRAAAGTSGSNHARIDAAEGSPDIPD 148  
|||||  
DB 61 RLPVDLAEELGHRDVARYLRAAAGTSGSNHARIDAAEGSPDIPD 105  
|||||

RESULT 34  
US-09-115-252-14  
Sequence 14, Application US/09115252  
Patent No. 6060301  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/115,252  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,810  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-115-252-14

Query Match 70.9%; Score 105; DB 3; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSAVAEILLHGAEPNCADPATLTTPVHDAAREGFLDTLVYLHRAGARLDVVDAMG 103  
|||||  
Db 1 MMGSAVAEILLHGAEPNCADPATLTTPVHDAAREGFLDTLVYLHRAGARLDVVDAMG 60  
|||||

QY 104 RLPPDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIPD 148  
|||||  
61 RLPPDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIPD 105  
|||||

RESULT 35  
US-08-986-515-14  
Sequence 14, Application US/08986515  
Patent No. 6090578  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/986,515  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/480,810  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-986-515-14

Query Match 70.9%; Score 105; DB 3; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSAVAEILLHGAEPNCADPATLTTPVHDAAREGFLDTLVYLHRAGARLDVVDAMG 103  
|||||  
Db 1 MMGSAVAEILLHGAEPNCADPATLTTPVHDAAREGFLDTLVYLHRAGARLDVVDAMG 60  
|||||

QY 104 RLPPDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIPD 148  
|||||  
61 RLPPDLAEELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIPD 105  
|||||

RESULT 36  
US-09-120-128-14  
Sequence 14, Application US/09120128  
Patent No. 6140473  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS2 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/120,128  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,047  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 14:



SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-120-128-14

Query Match 70.9%; Score 105; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVAELLHGAPNCADPATLTFRPVHDAREGFLDTLVLRHAGARLDVRDAMG 103  
|||||  
DB 1 MMGSARVAELLHGAPNCADPATLTFRPVHDAREGFLDTLVLRHAGARLDVRDAMG 60

QY 104 RLPVDLAEEIGHRDVARYLRAAAGTSGSNHARIDAEGSPDIDP 148  
|||||  
DB 61 RLPVDLAEEIGHRDVARYLRAAAGTSGSNHARIDAEGSPDIDP 105

RESULT 37

US-09-120-129-14  
Sequence 14, Application US/09120129

Patent No. 6180776

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander

TITLE OF INVENTION: MTS2 GENE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/120,129

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/486,047

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: PCT/US95/03316

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938

FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,086

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,369

FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
LENGTH: 105 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-120-129-14

Query Match 70.9%; Score 105; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVAELLHGAPNCADPATLTFRPVHDAREGFLDTLVLRHAGARLDVRDAMG 103  
|||||  
DB 1 MMGSARVAELLHGAPNCADPATLTFRPVHDAREGFLDTLVLRHAGARLDVRDAMG 60

QY 104 RLPVDLAEEIGHRDVARYLRAAAGTSGSNHARIDAEGSPDIDP 148  
|||||  
DB 61 RLPVDLAEEIGHRDVARYLRAAAGTSGSNHARIDAEGSPDIDP 105

RESULT 38

US-09-201-139-14  
Sequence 14, Application US/09201139

Patent No. 6210949

GENERAL INFORMATION:

APPLICANT: Stone, Steven

APPLICANT: Jiang, Ping

TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/201,139

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/508,735

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/03316

FILING DATE: 17-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24884-109348

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4848

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 105 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-201-139-14

Query Match 70.9%; Score 105; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVAEELLHGAEPNCADPATLTRPVHDAAREGFDLTLYVLRAGARLDVBDAMG 103  
DB 1 MMGSARVAEELLHGAEPNCADPATLTRPVHDAAREGFDLTLYVLRAGARLDVBDAMG 60  
QY 104 RLVPDLAEELGHRDVARYLRAAAGGTGSGNHARIDAEGPSDIPD 148  
DB 61 RLVPDLAEELGHRDVARYLRAAAGGTGSGNHARIDAEGPSDIPD 105

RESULT 39  
US-09-120-131-14  
; Sequence 14, Application US/09120131  
; Patent No. 6218146  
; GENERAL INFORMATION:  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: MTS2 GENE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/120,131  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/486,047  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: PCT/US95/03316  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/251,938  
; FILING DATE: 01-JUN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,087  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/215,086  
; FILING DATE: 18-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,369  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/214,582  
; FILING DATE: 18-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 24884-109348-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-8300  
; TELEFAX: 202-962-4810  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 105 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-120-131-14

Query Match 70.9%; Score 105; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1,1e-90;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 MMGSARVAEELLHGAEPNCADPATLTRPVHDAAREGFDLTLYVLRAGARLDVBDAMG 103  
DB 1 MMGSARVAEELLHGAEPNCADPATLTRPVHDAAREGFDLTLYVLRAGARLDVBDAMG 60  
QY 104 RLVPDLAEELGHRDVARYLRAAAGGTGSGNHARIDAEGPSDIPD 148  
DB 61 RLVPDLAEELGHRDVARYLRAAAGGTGSGNHARIDAEGPSDIPD 105

RESULT 40  
PCT-US96-05252-5  
; Sequence 5, Application PC/TUS9605252  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: p19: A Cell Cycle Inhibitor  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Stuart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/05252  
; FILING DATE: Not yet assigned  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,093  
; FILING DATE: 17-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen L.  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 02307B-059910PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..157  
; OTHER INFORMATION: /note="human p16"  
PCT-US96-05252-5

Query Match 64.2%; Score 95; DB 5; Length 157;  
Best Local Similarity 100.0%; Pred. No. 3.4e-81;  
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 LLLHGAEPNCADPATLTRPVHDAAREGFDLTLYVLRAGARLDVBDAMGRLPVDLAEEEL 113  
DB 63 LLLHGAEPNCADPATLTRPVHDAAREGFDLTLYVLRAGARLDVBDAMGRLPVDLAEEEL 122  
QY 114 GHRDVARYLRAAAGGTGSGNHARIDAEGPSDIPD 148  
DB 123 GHRDVARYLRAAAGGTGSGNHARIDAEGPSDIPD 157

RESULT 41  
US-08-581-918A-37  
; Sequence 37, Application US/08581918A  
; Patent No. 6043030

GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
TITLE OF INVENTION: Related Thereto  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Elliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordpad  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/581,918A  
FILING DATE: 02-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/497,214  
FILING DATE: 30-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/346,147  
FILING DATE: 29-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-071.06  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1299  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-581-918A-37

Query Match 60.1%; Score 89; DB 3; Length 89;  
Best Local Similarity 100.0%; Pred. No. 7.7e-76;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IOVMMGSAVAAELLLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVVD 100  
DB 1 IOVMMGSAVAAELLLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVVD 60

QY 101 AMGRLPVDLAEEELGHRDVARYLRAAAGT 129  
DB 61 AMGRLPVDLAEEELGHRDVARYLRAAAGT 89

RESULT 42  
US-08-346-147B-37  
Sequence 37, Application US/08346147B  
Patent No. 6211334  
GENERAL INFORMATION:  
APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannon, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
TITLE OF INVENTION: Related Thereto  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Elliot  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordpad  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/346,147B  
FILING DATE: 29-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-071.04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1299  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-346-147B-37

Query Match 60.1%; Score 89; DB 4; Length 89;  
Best Local Similarity 100.0%; Pred. No. 7.7e-76;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IOVMMGSAVAAELLLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVVD 100  
DB 1 IOVMMGSAVAAELLLHGAEPNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVVD 60

QY 101 AMGRLPVDLAEEELGHRDVARYLRAAAGT 129  
DB 61 AMGRLPVDLAEEELGHRDVARYLRAAAGT 89

## RESULT 43

US-08-581-918A-38  
; Sequence 38, Application US/08581918A  
; Patent No. 6043030  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley, Hoag & Eliot  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordpad  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/581,918A  
; FILING DATE: 02-JAN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/497,214  
; FILING DATE: 30-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/346,147  
; FILING DATE: 29-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/306,511  
; FILING DATE: 14-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/248,812  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,371  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/154,915  
; FILING DATE: 18-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1299  
; TELEFAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 88 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-581-918A-38

Query Match 48.6%; Score 72; DB 3; Length 88;  
Best Local Similarity 100.0%; Pred. No. 5.2e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IQVMMGSAKYAELLILHGAEPNCADPATLTTRPVHDAREGFLDTLVYLHRAGARLDVVD 100

Db 1 IQVMMGSAKYAELLILHGAEPNCADPATLTTRPVHDAREGFLDTLVYLHRAGARLDVVD 60  
QY 101 AMGRLPVDLAE 112  
Db 61 AMGRLPVDLAE 72

## RESULT 44

US-08-346-147B-38  
; Sequence 38, Application US/08346147B  
; Patent No. 6211334  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley, Hoag & Eliot  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordpad  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/346,147B  
; FILING DATE: 29-NOV-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/306,511  
; FILING DATE: 14-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/248,812  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,371  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/154,915  
; FILING DATE: 18-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1299  
; TELEFAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 88 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-346-147B-38

Query Match 48.6%; Score 72; DB 4; Length 88;  
Best Local Similarity 100.0%; Pred. No. 5.2e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IQVMMGSAKYAELLILHGAEPNCADPATLTTRPVHDAREGFLDTLVYLHRAGARLDVVD 100

Db 1 IQVMMGSA RVALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDV RD 60  
OY 101 AMGRLEPVDAEE 112  
Db 61 AMGRLEPVDAEE 72

RESULT 45  
PCT-US96-05252-6  
; Sequence 6, Application PC/TUS9605252  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: p19: A Cell Cycle Inhibitor  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/05252  
; FILING DATE: Not yet assigned  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,093  
; FILING DATE: 17-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen L.  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 02307B-059910PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..136  
; OTHER INFORMATION: /note="human p15"  
PCT-US96-05252-6

Query Match 48.6%; Score 72; DB 5; Length 136;  
Best Local Similarity 100.0%; Pred. No. 7.7e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 IQVMMGSA RVALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDV RD 100  
Db 49 IQVMMGSA RVALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDV RD 108  
OY 101 AMGRLEPVDAEE 112  
Db 109 AMGRLEPVDAEE 120

RESULT 46  
US-08-306-511A-4  
; Sequence 4, Application US/08306511A  
; Patent No. 5962316  
; GENERAL INFORMATION:

APPLICANT: Beach, David H.  
APPLICANT: Demetrick, Douglas J.  
APPLICANT: Serrano, Manuel  
APPLICANT: Hannou, Gregory J.  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
TITLE OF INVENTION: Related Thereto  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,511A  
FILING DATE: 14-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: CSI-001CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-306-511A-4

Query Match 48.6%; Score 72; DB 2; Length 137;  
Best Local Similarity 100.0%; Pred. No. 7.8e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 IQVMMGSA RVALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDV RD 100  
Db 50 IQVMMGSA RVALLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDV RD 109  
OY 101 AMGRLEPVDAEE 112  
Db 110 AMGRLEPVDAEE 121

RESULT 47  
US-08-893-274-4  
; Sequence 4, Application US/08893274  
; Patent No. 5968821  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannou, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,  
; TITLE OF INVENTION: and Uses Related Thereto  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII(text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,274  
FILING DATE: 15-JULY-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,511  
FILING DATE: 14-SEPTEMBER-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/248,812  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,371  
FILING DATE: 14-APRIL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/154,915  
FILING DATE: 18-NOVEMBER-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/991,997  
FILING DATE: 17-DECEMBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/963,308  
FILING DATE: 16-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV-071.09  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1000  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-893-274-4

Query Match 48.6%; Score 72; DB 2; Length 137;  
Best Local Similarity 100.0%; Pred. No. 7.8e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 41 IQVMMGSAVVAELLLHGAEPCADPATLTRPVHDAAREGFLDTLVYVLRAGARLDVVD 100  
DB 50 IQVMMGSAVVAELLLHGAEPCADPATLTRPVHDAAREGFLDTLVYVLRAGARLDVVD 109  
101 AMGRLPVDAEE 112  
110 AMGRLPVDAEE 121

RESULT 48  
US-08-474-177-16  
Sequence 16, Application US/08474177  
Patent No. 5624819  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
SOFTWARE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-177-16

Query Match 48.6%; Score 72; DB 1; Length 138;  
Best Local Similarity 100.0%; Pred. No. 7.8e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 41 IQVMMGSAVVAELLLHGAEPCADPATLTRPVHDAAREGFLDTLVYVLRAGARLDVVD 100  
DB 51 IQVMMGSAVVAELLLHGAEPCADPATLTRPVHDAAREGFLDTLVYVLRAGARLDVVD 110  
101 AMGRLPVDAEE 112  
111 AMGRLPVDAEE 122

RESULT 49  
US-08-487-033-16  
Sequence 16, Application US/08487033  
Patent No. 5739027  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1E1-Beta GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,033  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-487-033-16

Query Match 48.6%; Score 72; DB 1; Length 138;  
Best Local Similarity 100.0%; Pred. No. 7.8e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLVYLRAGARLDVRD 100  
|||||  
DB 51 IQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLVYLRAGARLDVRD 110  
|||||

QY 101 AMGRLPVDLAE 112  
|||||  
111 AMGRLPVDLAE 122

RESULT 50  
US-08-480-810-16  
Sequence 16, Application US/08480810  
Patent No. 5801236  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS1 GENE  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,810

FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03316  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-480-810-16

Query Match 48.6%; Score 72; DB 1; Length 138;  
Best Local Similarity 100.0%; Pred. No. 7.8e-60;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLVYLRAGARLDVRD 100  
|||||  
DB 51 IQVMMGSAVAVELLHGAEPNCADPATLTRPVHDAREGFLDTLVYLRAGARLDVRD 110  
|||||

QY 101 AMGRLPVDLAE 112  
|||||  
111 AMGRLPVDLAE 122

Search completed: September 19, 2002, 17:28:51  
Job time: 219 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:24:27 ; Search time 29.99 Seconds  
(without alignments)  
548.147 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 148  
Sequence: 1 MEPSADWLATAARGRVEEV.....TRGSNHARIDAEGSPDIP 148

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Wsize : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

A\_Geneseq\_032802:\*  
1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:\*  
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19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	100.0	148	16	AA81701 Multiple tumour su
2	148	100.0	148	16	AA80940 Human multiple tum
3	148	100.0	151	15	AA853401 Inhibitor of cycli
4	148	100.0	156	16	AA85116 Cell-cycle regulat
5	148	100.0	156	20	AA24741 Human TNK-4 protei
6	148	100.0	156	21	AA88354 Human cell cycle r
7	148	100.0	391	18	AAW2354 CDK inhibitory fus
8	148	100.0	391	20	AAW95094 Human p27-p16 fus
9	148	100.0	391	21	AA97526 Human W3 protein s
10	148	100.0	391	21	AA96041 Antiproliferative
11	148	100.0	391	21	AA96068 Angiogenesis inhib

#### ALIGNMENTS

RESULT 1  
ID AA81701 standard; Protein: 148 AA.  
XX

12	121	81.8	156	18	AAW10627	Tumour suppressor
13	121	81.8	156	18	AAW19251	Human multiple tum
14	121	81.8	156	19	AAW74549	Amino acid sequenc
15	121	81.8	156	19	AAW40524	Human MTS1 protein
16	121	81.8	156	20	AAW80524	A human multiple t
17	121	81.8	156	21	AA815498	Human MTS1 protein
18	121	81.8	156	21	AA97524	Human p16 protein
19	121	81.8	156	21	AA96053	Human cyclin depen
20	121	81.8	156	21	AA96067	Human cyclin depen
21	121	81.8	156	21	AA92921	Human multiple tum
22	121	81.8	156	21	AA91102	Human multiple tum
23	121	81.8	156	21	AA95945	Human MTS1 protein
24	121	81.8	156	21	AA94902	Human multiple tum
25	121	81.8	156	22	AAU02122	Human multiple tum
26	121	81.8	156	22	AAE01002	Human multiple tum
27	121	81.8	156	22	AA867334	Protein encoded by
28	121	81.8	156	22	AA836890	Human Multiple Tum
29	121	81.8	228	21	AA97522	Human W3 protein s
30	121	81.8	228	21	AA96051	Antiproliferative
31	121	81.8	228	21	AA96078	Angiogenesis inhib
32	121	81.8	237	20	AAW95105	Truncated p27/p16
33	121	81.8	237	21	AAW97534	Human W9 protein s
34	121	81.8	237	21	AA96049	Antiproliferative
35	121	81.8	237	21	AA96076	Angiogenesis inhib
36	121	81.8	252	20	AAW95106	Truncated p27/p16
37	121	81.8	252	21	AA97535	Human W10 protein
38	121	81.8	252	21	AA96050	Antiproliferative
39	121	81.8	252	21	AA96077	Angiogenesis inhib
40	121	81.8	323	21	AA96079	Secretable angio
41	121	81.8	334	20	AAW95103	Truncated p27/p16
42	121	81.8	334	20	AAW97532	Human W8 protein s
43	121	81.8	334	21	AA96047	Antiproliferative
44	121	81.8	334	21	AA96074	Angiogenesis inhib
45	121	81.8	365	18	AAW23536	CDK inhibitory fus
46	121	81.8	365	20	AAW95107	Human p16p27 fusio
47	121	81.8	365	20	AAW95096	Human p16p27 fusio
48	121	81.8	365	21	AA97527	Human W4 protein s
49	121	81.8	365	21	AA97529	Human W6 protein s
50	121	81.8	365	21	AA96042	Antiproliferative
51	121	81.8	365	21	AA96044	Angiogenesis inhib
52	121	81.8	365	21	AA96069	Angiogenesis inhib
53	121	81.8	365	21	AA96071	Angiogenesis inhib
54	121	81.8	380	18	AAW23535	CDK inhibitory fus
55	121	81.8	380	20	AAW95095	Human p16(GS)p27 f
56	121	81.8	380	21	AA97528	Human W5 protein s
57	121	81.8	380	21	AA96043	Antiproliferative
58	121	81.8	380	21	AA96070	Angiogenesis inhib
59	120	81.1	337	21	AA96080	Secretable angio
60	115	77.7	172	22	AAU02966	Angiotensin conver
61	112	75.7	156	22	AAE01008	Human multiple tum
62	105	70.9	105	16	AA81700	Multiple tumour su
63	105	70.9	105	16	AA80947	Human multiple tum
64	105	70.9	105	18	AAW19254	Human multiple tum
65	105	70.9	105	19	AAW74550	Amino acid sequenc
66	105	70.9	105	19	AAW40525	Human MTS1-beta
67	105	70.9	105	20	AAW80525	Human MTS1-beta
68	105	70.9	105	21	AA815500	A human multiple t
69	105	70.9	105	21	AA92922	Human MTS1beta p
70	105	70.9	105	21	AA91103	Human multiple tum
71	105	70.9	105	21	AA959416	Human MTS1beta p
72	105	70.9	105	21	AA954923	Human multiple tum
73	105	70.9	105	22	AAU02123	Human multiple tum
74	105	70.9	105	22	AAE01004	Human multiple tum
75	105	70.9	105	22	AA867335	Human multiple tum

```

AC AAR81701;
XX
DE 08-MAY-1996 (first entry)
XX
DE Multiple tumour suppressor 1 (MTS1) polypeptide.
XX
DE Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
XX
DE predilection; melanoma; leukaemia; lymphoma; prognosis;
XX
DE pancreas; breast; thyroid.
XX
OS Homo sapiens.
XX
PN W09525813-A1.
XX
PD 28-SEP-1995.
XX
PF 17-MAR-1995; 95MO-US03537.
XX
PR 01-JUN-1994; 94US-0251938.
XX
PR 18-MAR-1994; 94US-0214581.
XX
PR 18-MAR-1994; 94US-0215086.
XX
PR 18-MAR-1994; 94US-0215087.
XX
PR 14-APR-1994; 94US-0227369.
XX
PA (MYRI-) MYRIAD GENETICS INC.
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Cannon-Albright LA, Kamb A, Skolnick MH;
XX
DR WPI: 1995-344626/44.
XX
DR N-PSDB; AAT00736.
XX
PT Detecting polymorphism associated with cancer pre:disposition - also
PT DNA, vectors and host cells e.g. for gene or protein replacement
PT therapy and drug screening
XX
PS Example 8: Pages 92-93; 148pp; English.
XX
CC An individual can be diagnosed as having a predisposition to cancer
CC by detecting an alteration in the wild type multiple tumour
CC suppressor (MTS) gene, using gene probes which hybridise to the MTS1
CC gene ORF AAT00736 (which encodes AAR81701) mutant sequences AAT00749/50.
CC The above assay can also be used in the diagnosis and prognosis of
CC melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
CC cancers, etc..
XX
SQ Sequence 148 AA;

```

Query Match 100.0%; Score 148; DB 16; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.5e-134;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MEPSADWLATAAARGVEEVRALLLEAVALPNAPNSYGRPTQVMMGSAARYAELLHLHGA 60
DB 1 mepsadwlataaargveevrallleavalpnapsygrptqvmmgसार्याएल्लहगा 60
QY 61 EPNCADEPTLTTPVYHDAARBEGLDTLVYLRAGARLDVRODAGRLPVDLAEELGHRDVAR 120
DB 61 epcnadepalttrpvhdaaregfltdltvylhragarldvrdawgrlpvdlaeelghrdvar 120
QY 121 YLRAAAGTGRGSNHARIDAEGSPDIPD 148
DB 121 ylr aaagtgtrgsnharidaaegpsdipd 148

```

RESULT 2  
AAR80940  
ID AAR80940 standard; Protein: 148 AA.  
AC AAR80940;  
XX  
XX 03-MAY-1996 (first entry)

```

XX
DE Human multiple tumour suppressor polypeptide, MTS1.
XX
DE Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;
XX
DE astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
XX
DE gene therapy; chronic.
XX
OS Homo sapiens.
XX
PN W09525429-A1.
XX
PD 28-SEP-1995.
XX
PF 17-MAR-1995; 95MO-US03316.
XX
PR 01-JUN-1994; 94US-0251938.
XX
PR 18-MAR-1994; 94US-0214581.
XX
PR 18-MAR-1994; 94US-0214582.
XX
PR 18-MAR-1994; 94US-0215088.
XX
PR 14-APR-1994; 94US-0227369.
XX
PR 18-MAR-1994; 94US-0215086.
XX
PR 18-MAR-1994; 94US-0215087.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Kamb A;
XX
DR WPI: 1995-344401/44.
XX
DR N-PSDB; AAO9158.
XX
PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences
PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.
PT melanoma or leukaemia
XX
PS Claim 5: Page 92-93; 156pp; English.
XX
CC Several multiple tumour suppressor (MTS) polypeptides have been
CC isolated and sequenced. This sequence is the MTS polypeptide MTS1
CC MTS polypeptide-encoding cDNAs and mutants of these are useful for
CC the diagnosis or prognosis of human cancer. Germ-line mutations of
CC MTS cDNAs can be used for diagnosing predisposition to melanoma,
CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's
CC lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus,
CC testis, kidney, stomach and rectum. The wild-type gene is useful
CC for gene therapy and MTS polypeptides may also be used for protein
CC replacement therapy. Also the polypeptides or cells contg. an
CC altered MTS gene are useful for screening for potential cancer
CC therapeutics.
XX
SQ Sequence 148 AA;

```

Query Match 100.0%; Score 148; DB 16; Length 148;  
Best Local Similarity 100.0%; Pred. No. 1.5e-134;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MEPSADWLATAAARGVEEVRALLLEAVALPNAPNSYGRPTQVMMGSAARYAELLHLHGA 60
DB 1 mepsadwlataaargveevrallleavalpnapsygrptqvmmgसार्याएल्लहगा 60
QY 61 EPNCADEPTLTTPVYHDAARBEGLDTLVYLRAGARLDVRODAGRLPVDLAEELGHRDVAR 120
DB 61 epcnadepalttrpvhdaaregfltdltvylhragarldvrdawgrlpvdlaeelghrdvar 120
QY 121 YLRAAAGTGRGSNHARIDAEGSPDIPD 148
DB 121 ylr aaagtgtrgsnharidaaegpsdipd 148

```

RESULT 3  
AAR53401  
ID AAR53401 standard; Protein: 151 AA.  
XX



```

DT 23-AUG-1999 (first entry)
XX
DE Human INK-4 protein p16.
XX
KM INK-4; p16; p18; p19; CDK4; cell cycle regulatory protein;
XX transgenic mouse; p16-INK4-a; carcinogen; anti-proliferative.
XX
OS Homo sapiens.
XX
PN US919997-A.
XX
PD 06-JUL-1999.
XX
PF 04-APR-1996; 96US-0627610.
XX
PR 04-APR-1996; 96US-0627610.
XX 18-NOV-1993; 93US-0154915.
XX 14-APR-1994; 94US-0227371.
XX 25-MAY-1994; 94US-0248812.
XX 14-SEP-1994; 94US-0306511.
XX 29-NOV-1994; 94US-0346147.
XX 30-JUN-1995; 95US-0497214.
XX 02-JAN-1996; 96US-0581918.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI Beach DH, DePinho RA, Serrano M;
XX
DR WPI; 1999-394656/33.
XX N-PSDB; AAX80472.
XX
PT Transgenic mice with modified cell-cycle regulation
XX
PS Disclosure: Column 45-46; 35pp; English.
XX
CC The present invention describes a transgenic mouse having germline and
CC somatic cells which comprise an incorporated transgene that disrupts and
CC inhibits the p16-INK4-a gene leading to tumour susceptibility. Also
CC described is a method of making a mouse and mouse embryonic stem cells a
CC functionally disrupted p16-INK4-a gene which comprises transferring a
CC transgene construct into embryonic stem cells of a mouse and
CC transferring these into a mouse blastocyst and implanting the resulting
CC chimeric blastocyst into a female mouse selecting offspring having an
CC endogenous p16-INK4-a gene allele. The transgenic mouse is useful for
CC evaluating the carcinogenic potential or the anti-proliferative activity
CC of a test compound. The present sequence represents the human INK4
CC protein p16 given in the present invention.
CC
Sequence 156 AA:
Query Match 100.0%; Score 148; DB 20; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-134;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPSADMLATAAARGVEEVRALLLEAVLPNAPNSYGRRIQVMMGSAVVELLLHGA 60
DB 9 mepsadwlataaargveevrallleavlpnapnsygrripdyvmmgssarvaellllhga 68
QY 61 EPNCADPATLTPRVHDAREGFLLDTLVVLRAGARLDVDRAGKLPVDLAEELGHRDYAR 120
DB 69 epcnadpatltprvhdaregflldtlvvlragsarldvdragrllpvdlaeelgrrdyar 128
QY 121 YLRAAGGTRGSHHARIDAEGSPDIP 148
DB 129 ylrraaggtgrshharidaaegpsdip 156
XX
RESULT 6
AAY88354
ID AAY88354 standard; Protein; 156 AA.
XX

```

```

AC AAY88354;
XX
DT 14-JUL-2000 (first entry)
XX
DE Human cell cycle regulatory protein p16 amino acid sequence.
XX
KM Cell cycle regulatory protein; CCR; p16; diagnostic assay; detection;
XX cell proliferation; differentiation; neoplasia; cancer; cell growth;
XX cyclin-dependent kinase inhibitor; CDK; human; chromosome 9p21-22.
XX
OS Homo sapiens.
XX
PN US6043030-A.
XX
PD 28-MAR-2000.
XX
PF 02-JAN-1996; 96US-0581918.
XX
PR 17-DEC-1992; 92US-0991997.
XX 18-NOV-1993; 93US-0154915.
XX 14-APR-1994; 94US-0227371.
XX 25-MAY-1994; 94US-0248812.
XX 14-SEP-1994; 94US-0306511.
XX 29-NOV-1994; 94US-0346147.
XX 30-JUN-1995; 95US-0497214.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Beach DH, Demetrick DJ, Serrano M, Hannon GJ;
XX
DR WPI; 2000-270336/23.
XX N-PSDB; AAA13096.
XX
PT Use of a mammalian cell cycle regulatory protein (a CDK-inhibitory
PT protein) in a diagnostic assay for identifying a cell at risk for a
PT disorder characterized by unwanted cell proliferation or
PT differentiation.
XX
PS Claim 14; Column 57-58; 61pp; English.
XX
CC This sequence represents the human cell cycle regulatory protein (CCR)
CC p16 amino acid sequence. The p16 gene is located on chromosome 9p21-22.
CC The invention relates to a diagnostic assay which comprises detecting a
CC mutation in the p16 gene, which is used to identify a cell or cells at
CC risk of developing a disorder characterised by unwanted cell
CC proliferation or differentiation. p16 is a cyclin-dependent kinase
CC (CDK)-inhibitory protein, and functions as an inhibitor of cell-cycle
CC progression and ultimately cell growth. The assay can be used for
CC identifying a cell or cells at risk for a disorder (neoplasia)
CC characterized by unwanted cell proliferation or differentiation. The
CC method is used for detecting mutations in either a CCR gene or CDK gene
CC which alter complex formation between these two proteins. The method is
CC also used for detecting mutations in other cellular proteins which
CC disrupt protein interactions such as mutations which disrupt binding of
CC the p3 protein with other cellular proteins, e.g. Wilm's tumour
CC suppressor protein WT1. They can also be used to detect mutations in
CC pairs of signal transduction proteins such as ras protein or other
CC cellular proteins which interact with ras, e.g. ras GTPase activating
CC proteins (GAPs). The method is convenient for detecting mutants of CCR
CC genes encoding proteins which are unable to physically interact with a
CC CDK bait protein.
XX
Sequence 156 AA:
Query Match 100.0%; Score 148; DB 21; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-134;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPSADMLATAAARGVEEVRALLLEAVLPNAPNSYGRRIQVMMGSAVVELLLHGA 60
DB 9 mepsadwlataaargveevrallleavlpnapnsygrripdyvmmgssarvaellllhga 68
XX

```

```

QY 61 EPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVARDAMGRLPVDLAELGHRDVAR 120
    |||||||
Db 69 epncadpatitlrpvhdaaregfltdltvlhragarlvdardawgripvdaaeelghrdvar 128
QY 121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
    |||||||
Db 129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156

RESULT 7
AAW23534
ID AAW23534 standard; Protein: 391 AA.
XX
AC AAW23534;
XX
DT 16-MAR-1998 (first entry)
XX
DE CDK inhibitory fusion protein #1.
XX
KW Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;
KW chimeric polypeptide; human; binding motif; proliferation control;
KW cell differentiation; cell-cycle inhibitor; proliferative disorder;
KW tissue degeneration; therapy.
XX
OS Homo sapiens.
XX
EH Key Location/Qualifiers
FT Misc-difference 1..7
FT /note= "poly-His tag"
FT Misc-difference 205..219
FT /note= "(GlySer)2 linker"
XX
PN WO9727297-A1.
XX
PD 31-JUL-1997.
XX
PF 17-JAN-1997; 97WO-US00569.
XX
PR 23-JAN-1996; 96US-0589981.
XX
PA (MITO-) MITOTIX INC.
XX
PI Beach D, Gyuris J, Lamphere L;
XX
DR WPI: 1997-393685/36.
DR N-PSDB; AAT74051.
XX
PT Chimeric inhibitor of cyclin dependent kinase - useful for gene
PT therapy of cancer and other proliferative and differentiative
PT diseases
XX
PS Claim 40; Page 38-40; 58pp; English.
XX
CC This sequence represents a chimeric polypeptide of the invention. It was
CC derived from a fusion of the human p27 and p16 cDNA sequences. The
CC chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)
CC binding motifs from at least two different proteins that bind to CDKs.
CC The protein controls proliferation and/or differentiation of cells,
CC particularly they inhibit cell-cycle progression. They can be used to
CC treat a wide range of proliferative disorders, e.g. cancer, leukemia,
CC psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They
CC can also treat diseases associated with de-differentiation or
CC degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's
CC diseases, gastric ulcers and autonomous diseases of the peripheral
CC nervous system. Other applications include reducing growth of hair and
CC protecting hair follicle cells against cytotoxic treatments, cosmetically
CC to treat various forms of folliculitis, and to inhibit spermatogenesis or
CC oogenesis. The chimeric proteins can also be used in vitro to maintain
CC cells, especially neurons intended for testing specific activity of
CC trophic factors, at selected points in the cell cycle. The proteins are
CC more active inhibitors of the CDK/cyclin complex than binding motifs used
CC individually (since they may bind to CDK involved in different stages of
CC the cell cycle).

```

```

XX SQ Sequence 391 AA;
QY 1 MEPSADWLATAAARGVEEYRALLEAVALPNAPNSYGRRPICVMMGSAVLELLHGA 60
    |||||||
Db 244 mepsadwlataaargveeyrallaevalpnepnsgyrrpdygmungsarvaellllhga 303
QY 61 EPNCADPATITRPVHDAAREGFLDTLVVLRAGARLDVARDAMGRLPVDLAELGHRDVAR 120
    |||||||
Db 304 epncadpatitlrpvhdaaregfltdltvlhragarlvdardawgripvdaaeelghrdvar 363
QY 121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
    |||||||
Db 364 YLRAAAGGTRGSNHARIDAAEGPSDIPD 391

RESULT 8
AAW95094
ID AAW95094 standard; Protein: 391 AA.
XX
AC AAW95094;
XX
DT 25-MAY-1999 (first entry)
XX
DE Human p27-p16 fusion protein.
XX
KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW tachycardia; human; p27; p16.
XX
OS Homo sapiens.
XX
PN WO9906540-A2.
XX
PD 11-FEB-1999.
XX
PF 29-JUL-1998; 98WO-US15759.
XX
PR 29-JUL-1997; 97US-0902572.
XX
PA (MITO-) MITOTIX INC.
XX
PI Beach DH, Gyuris J, Lamphere L;
XX
DR WPI: 1999-153770/13.
DR N-PSDB; AAX26220.
XX
PT Fusion and chimaeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
XX
PS Claim 63; Page 70-72; 88pp; English.
XX
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic

```

CC polypeptide sequence (TP) from an intracellular protein that alters a  
CC cellular process when FP enters the cell, and (ii) a transcellular  
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP  
CC consists of at least one CDK-binding motif and a TCP. (A) are used to  
CC treat vascular wounds that involve a break in the endothelium and  
CC excessive proliferation of smooth muscle, particularly restenosis but  
CC more generally any repair of cardiovascular damage, arteriosclerotic  
CC lesions or for endothelialisation of synthetic vascular grafts. More  
CC generally, FP are used to treat unwanted cellular proliferation in a very  
CC wide range of situations, e.g. for treating vascular diseases as above;  
CC fibrotic disorders (e.g. rheumatoid arthritis, diabetes, cirrhosis); many  
CC tumours (gliomas, leukemias); chronic inflammation; neurodegeneration;  
CC acne; also to control hair growth (e.g. to prevent hair loss caused by  
CC chemotherapy or radiation); periodontal disease; to treat tachycardia;  
CC to inhibit spermatogenesis etc. Chimeric proteins comprising CDK-binding  
CC motifs from two or more different proteins bind to CDKs so inhibit cell  
CC cycle progression, particularly smooth muscle cell proliferation. The  
CC gene constructs may also be used to produce FP in cell cultures, for  
CC production or for regulating cell differentiation in vitro. The present  
CC sequence represents a human p27-p16 fusion protein.

Sequence 391 AA:

Query Match 100.0%; Score 148; DB 20; Length 391;  
Best Local Similarity 100.0%; Pred. No. 3.8e-134;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADMATTAARGVVEVRALLEAVALPNAPNSYGRRPQVMMGSAARVAELLHLGA 60  
|  
DB 244 mepsadwlataaargvvevrallleavallpnapsygrtrpqvmmgssarvae11llhga 303  
QY 61 EPNCADPATITFRVNDAAAREGFLDTLVYLHRAGARLDVNDAGRPLPYDLAEELGHRDVAR 120  
|  
DB 304 epcncadpatitlfrvndaaaregfldtlvylhragarldvndagrplpydlaeelghrdvar 363  
QY 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148  
|  
DB 364 ylraaagtrgsnharidaaegpsdipd 391

RESULT 9

AA97526 AAY97526 standard; Protein; 391 AA.

XX AAY97526;

XX 15-JAN-2001 (first entry)

XX Human W3 protein sequence.

KW Human: chimeric cyclin dependent kinase inhibitor; CDK1; therapy;  
KW adenovirus E4 protein; neoplasia; W3 protein.

OS Homo sapiens.

PN WO20052184-A1.

PD 08-SEP-2000.

PF 01-MAR-2000; 2000WO-US05350.

PR 01-MAR-1999; 99US-0122974.

PR 08-APR-1999; 99US-0128271.

PR 09-APR-1999; 99US-0128515.

PA (CELL-) CELL GENESYS INC.

PI (MITO-) MITOTIX INC.

PI Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;

DR WPI; 2000-587315/55.

DR N-PSDB; #AA90923.

XX protein and nucleic acid compositions for preventing and treating  
PT neoplasias (particularly cancer), comprises a novel chimeric cyclin  
PT dependent kinase inhibitor and adenovirus E4 protein -  
PS  
PS Example 1; Page 108-109; 126pp; English.

CC This sequence represents the human W3 protein.  
CC The invention relates to a protein composition comprising a novel  
CC purified chimeric cyclin dependent kinase inhibitor (CDK1) and a  
CC or the DNA encoding it are useful for treating neoplasias in animals. The  
CC compositions also find use in assays to eliminate a specific  
CC sub-population of cultured cells, to determine the susceptibility of  
CC neoplastic cells to treatment with the compositions and also in assays to  
CC synchronise cell growth in cultured cells.

SQ Sequence 391 AA:

Query Match 100.0%; Score 148; DB 21; Length 391;  
Best Local Similarity 100.0%; Pred. No. 3.8e-134;  
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSADMATTAARGVVEVRALLEAVALPNAPNSYGRRPQVMMGSAARVAELLHLGA 60  
|  
DB 244 mepsadwlataaargvvevrallleavallpnapsygrtrpqvmmgssarvae11llhga 303  
QY 61 EPNCADPATITFRVNDAAAREGFLDTLVYLHRAGARLDVNDAGRPLPYDLAEELGHRDVAR 120  
|  
DB 304 epcncadpatitlfrvndaaaregfldtlvylhragarldvndagrplpydlaeelghrdvar 363  
QY 121 YLRAAGGTRGSNHARIDAAEGPSDIPD 148  
|  
DB 364 ylraaagtrgsnharidaaegpsdipd 391

RESULT 10

AA96041 AAY96041 standard; Protein; 391 AA.

XX AAY96041;

XX 05-DEC-2000 (first entry)

XX Antiproliferative p27-p16 fusion protein W3.

XX

KW Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;  
KW p16; human; smooth muscle cell; hyperproliferation; restenosis;  
KW vasotropic; antiproliferative; gene therapy.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Location/Qualifiers

Peptide 1..7

Protein /label= 6His\_tag

Peptide /label= 8..204

Protein /label= p27

Peptide 205..219

Protein /label= Hinge

Protein 239..391

Protein /label= p16

WO20052159-A1.

08-SEP-2000.

28-FEB-2000; 2000WO-US04971.

01-MAR-1999; 99US-0122974.

05-NOV-1999; 99US-0163682.

09-DEC-1999; 99US-0457568.

```

XX (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX
XX Mcarthur J, Gyuris J, Finer M;
DR WPI: 2000-594183/56.
DR N-PSDB; AAA50488.
XX
PT Novel recombinant lentivirus for inhibiting proliferation of smooth
PT muscle cells in e.g. restenosis, is replication deficient and comprises
PT a transgene encoding a cyclin dependent kinase inhibitor -
XX
PS Example 1; Page 101-103; 126pp; English.
XX
XX The present sequence is that of p27-p16 fusion protein W3 comprising
XX an N-terminal 6His tag, the human p27 protein (see AAY96052), a
XX (Gly4Ser)3 hinge and the human p16 protein (see AAY96053). It is
XX encoded by a nucleic acid obtained by PCR amplification of p27 and
XX p16 DNAs using primers that also included codons for the tag/hinge
XX regions. A claimed method for inhibiting smooth muscle cell
XX hyperproliferation involves transducing smooth muscle cells with a
XX replication-deficient recombinant adenovirus that lacks functional
XX E1 and E4 regions, and comprises a transgene encoding a cyclin
XX dependent kinase inhibitor (CDK1). The CDK1 is selected from an
XX INK4 family protein such as human p16, a CIP/KIP family protein
XX such as p27, active fragments of these, or fusion proteins
XX comprising (active fragments of) an INK4 family protein and a
XX CIP/KIP family protein (see AAY96046 and AAY96049). The method is used
XX to inhibit mammalian smooth muscle cell hyperproliferation, induced
XX by injury caused by angioplasty, stent placement or vein
XX engraftment. It is useful for treating vascular pathologies e.g.,
XX restenosis. Also claimed are recombinant lentiviruses encoding
XX CDK1s.
XX
SQ Sequence 391 AA:

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XX Key Location/Qualifiers
FH Peptide 1..7
FT /label= 6His_tag
FT Protein 8..204
FT /label= p27
FT Peptide 205..219
FT /label= Hinge
FT Protein 239..391
FT /label= p16
XX
XX WO200052158-A1.
XX
XX 08-SEP-2000.
XX
XX 28-FEB-2000; 2000WO-US04970.
XX
XX 01-MAR-1999; 99US-0122974.
XX 05-NOV-1999; 99US-0163682.
XX 09-DEC-1999; 99US-0457646.
XX
XX (CELL-) CELL GENESYS INC.
XX (MITO-) MITOTIX INC.
XX
XX Patel S, Mcarthur J, Gyuris J;
XX
XX WPI: 2000-565501/52.
XX N-PSDB; AAA50523.
XX
XX The present sequence is that of p27-p16 fusion protein W3
XX comprising an N-terminal 6His tag, the human p27 protein (see
XX AAY96066), a (Gly4Ser)3 hinge, and the human p16 protein (see
XX AAY96067). The fusion protein is encoded by a nucleic acid (see
XX AAA50523) that was obtained by PCR amplification of human p27 and p16
XX DNAs using primers that also included codons encoding the tag/hinge
XX regions of the fusion protein. A claimed method for inhibiting
XX angiogenesis involves transducing an epithelial cell with a
XX transgene encoding a cell dependent kinase inhibitor (CDK1). The
XX delivery system for the transgene is a liposome or a recombinant
XX virus. The CDK1 is a protein of the CIP/KIP family such as p27, a
XX protein of the INK4 family such as p16, active fragments of these
XX proteins, or a fusion of 2 CDK1 proteins such as p27 and p16. The
XX method is useful in treating conditions associated with angiogenesis,
XX such as neoplasia, rheumatoid arthritis, endometriosis, psoriasis
XX and vascular retinopathy (claimed). Alternatively, the transgene
XX is delivered to an auxiliary cell, and is expressed by that cell
XX such that the CDK1 is released into the blood and contacts the
XX target epithelial cell. The p27-p16 fusion proteins interact with
XX CDK4/cyclinD, CDK2/cyclinA and CDK2/cyclinE and inhibit cell cycle
XX progression.
XX
XX Sequence 391 AA:

```

```

RESULT 11
ID AAY96068 standard; Protein; 391 AA.
XX
XX AAY96068;
AC
XX
XX 05-DEC-2000 (first entry)
XX
XX Angiogenesis inhibitor (p27-p16 fusion) W3.
XX
XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; INK4; p27; p16;
XX human; angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;
XX endometriosis; psoriasis; vascular retinopathy; cytostatic;
XX antiarthritic; antineumatic; gynaecological; antipsoriatic;
XX antiproliferative; gene therapy.
XX
XX Homo sapiens.
OS Synthetic.

```

```

Query Match 100.0%; Score 148; DB 21; Length 391;
Best Local Similarity 100.0%; Pred. No. 3.8e-134;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 121 YLRAAAGTGRGSHARIDAAGPSDIP 148  
 |||||  
 Db 364 ylrAaagtrgsnharidaaegpsdip 391

## RESULT 12

AAW10627  
 ID AAW10627 standard; Protein; 156 AA.

AC AAW10627;

DT 28-OCT-1997 (first entry)

DE Tumour suppressor p16.

KM Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;  
 cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;  
 anti-angiogenic activity; hyperproliferative disorder.

OS Homo sapiens.

WO9703635-A2.

PD 06-FEB-1997.

PF 17-JUL-1996; 96WO-US11787.

PR 17-JUL-1995; 95US-0502881.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Jin X, Roth J;

DR WPI: 1997-132336/12.

N-PSDB; AAT60951.

PT Expression construct contg. DNA for tumour suppressor p16 - to  
 restore p16 activity to transformed cells, useful for treating lung  
 or bladder cancer or melanoma

PS Disclosure: Fig 1b; 92pp; English.

XX This sequence represents the tumour suppressor p16. The DNA encoding  
 CC this sequence is joined to a promoter functional in eukaryotic cells and  
 CC used in the expression construct of the invention. p16 is an inhibitory  
 CC subunit, which is involved in the control of cyclin-dependent kinase 4  
 CC activity, and functions as a tumour suppressor. By detecting this  
 CC sequence or the DNA encoding it, cancer cells can be detected. When the  
 CC nucleic acid molecule is in the sense orientation, the expression  
 CC construct can be used to restore p16 function in a cell, particularly by  
 CC reversing the transformed phenotype in tumours, especially lung or  
 CC bladder cancer or melanoma. It may also have anti-angiogenic activity,  
 CC and inhibit hyperproliferative disorders, e.g. restenosis. When the  
 CC nucleic acid molecule is inserted in the antisense orientation, the  
 CC expression construct inhibits p16 function. Reduced or increased levels  
 CC of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by  
 CC Southern or Northern blot, antibody immunoblot, fluorescent cell sorting  
 CC or immunoassay.

SO Sequence 156 AA.

## Query Match

Best Local Similarity 81.8%; Score 121; DB 18; Length 156;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRRIQYMMGSAFYAELLHGAEPNCADPATLTPYHDAAREGFLDTLV 87  
 |||||  
 Db 36 alpnapnsygrripqymmgasrvaellllhgaepncadpatlttrpyhdaaregfltdtlv 95  
 OY 88 VLRAGARLDVDRAMGRLLPVDLAEELGHRDVARYLRAAAGTGRGSHARIDAAGPSDIP 147  
 |||||  
 Db 96 vlhRagARldvdrAwgrlpvdlAeelghrdvArYlraaAgtrgsnharidaaegpsdip 155

OY 148 D 148  
 |  
 Db 156 d 156

## RESULT 13

AAW19251  
 ID AAW19251 standard; Protein; 156 AA.

AC AAW19251;

DT 10-SEP-1997 (first entry)

DE Human multiple tumour suppressor 1 gene product.

KM Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.  
 OS Homo sapiens.

PN US5624819-A.

PD 29-APR-1997.

PF 18-MAR-1994; 94US-0214582.

PR 07-JUN-1995; 95US-0474177.

PR 18-MAR-1994; 94US-0214582.

PR 18-MAR-1994; 94US-0215086.

PR 18-MAR-1994; 94US-0215087.

PR 14-APR-1994; 94US-0227369.

PR 01-JUN-1994; 94US-0251938.

PR 17-MAR-1995; 95WO-US03537.

PA (MYRI-) MYRIAD GENETICS INC.

PI (UTAH ) UNIV UTAH RES FOUND.

PI Cannon-Albright LA, Kamb A, Skolnick MH;

DR WPI: 1997-258217/23.

N-PSDB; AAT72311.

PT Human mutant multiple tumour suppressor gene sequences - for  
 production of recombinant mutant polypeptide(s)

PS Claim 1: Columns 61-64; 72pp; English.

XX The present sequence the human multiple tumour suppressor 1  
 CC (MTS1) gene product, useful in cancer diagnosis.

SO Sequence 156 AA;

## Query Match

Best Local Similarity 81.8%; Score 121; DB 18; Length 156;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRRIQYMMGSAFYAELLHGAEPNCADPATLTPYHDAAREGFLDTLV 87  
 |||||  
 Db 36 alpnapnsygrripqymmgasrvaellllhgaepncadpatlttrpyhdaaregfltdtlv 95  
 OY 88 VLRAGARLDVDRAMGRLLPVDLAEELGHRDVARYLRAAAGTGRGSHARIDAAGPSDIP 147  
 |||||  
 Db 96 vlhRagARldvdrAwgrlpvdlAeelghrdvArYlraaAgtrgsnharidaaegpsdip 155  
 OY 148 D 148  
 |  
 Db 156 d 156  
 RESULT 14  
 AAW74549  
 ID AAW74549 standard; Protein; 156 AA.



```
XX AAW74549;
AC 04-DEC-1998 (first entry)
DT
XX
XX Amino acid sequence of multiple tumour suppressor 1.
DE
XX Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
KW somatic mutation; gene therapy.
XX
XX Homo sapiens.
OS
XX US5801236-A.
PN
XX 01-SEP-1998.
PD
XX
XX 07-JUN-1995; 95US-0480810.
PF
XX
PR 07-JUN-1995; 95US-0480810.
PR 18-MAR-1994; 94US-0214582.
PR 18-MAR-1994; 94US-0215086.
PR 18-MAR-1994; 94US-0215087.
PR 14-APR-1994; 94US-0227369.
PR 01-JUN-1994; 94US-0251938.
PR 17-MAR-1995; 95WO-US03316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA
XX
XX Kamb A;
PI
XX
XX WPI: 1998-494842/42.
DR N-PSDB; AAV53819.
XX
XX Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
XX
XX Disclosure; Column 63-64; 73pp; English.
XX
XX This is the amino acid sequence of the multiple tumour suppressor 1
CC (MTS-1) protein, used in the method of the invention. The MTS gene
CC is useful in the diagnosis and prognosis of human cancer. e.g. by
CC standard nucleic hybridisation techniques, of patient samples. The
CC mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
XX
XX Sequence 156 AA:
SQ
Query Match 81.8%; Score 121; DB 19; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 ALPNAPNSYGRPIQVMMGSAFYAEILLHGAEPCADPATLTRPVHDAAREGFIDTLV 87
DB 36 alpnapnsygrripqymmgasrvaellllhgaeppcadpatltrpvhdaaregfldtlv 95
QY 88 VLHRAGARLDVDRDAMGRPLVDLAEEIGHRDVARYLRAAAGTSGSNHARIDAAGPSDIP 147
DB 96 vlhragarldvdrdawgrlpvdlaeelghrdvarylraaagtrsgsnharidaaegpsdip 155
QY 148 P 148
DB 156 d 156
```

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RESULT 15
AAW40524
ID AAW40524 standard; Protein; 156 AA.
XX
XX AAW40524;
AC
XX 15-JUL-1998 (first entry)
DT
XX
XX Human MTS1 protein.
DE
XX
XX MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
KW familial melanoma locus; MLM; predisposition.
XX
XX Homo sapiens.
OS
XX US5739027-A.
PN
XX 14-APR-1998.
PD
XX
XX 07-JUN-1995; 95US-0487033.
PF
XX
PR 07-JUN-1995; 95US-0487033.
PR 18-MAR-1994; 94US-0214582.
PR 18-MAR-1994; 94US-0215086.
PR 18-MAR-1994; 94US-0215087.
PR 14-APR-1994; 94US-0227369.
PR 01-JUN-1994; 94US-0251938.
PR 17-MAR-1995; 95WO-US03316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA
XX
XX Kamb A;
PI
XX
XX WPI: 1998-250421/22.
DR N-PSDB; AAV11238.
XX
XX DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
PT useful for the diagnosis of cancers related to MTS1E1-beta
PT mutation(s) and their treatment
XX
XX Disclosure; Column 63-64; 72pp; English.
XX
XX This sequence represents a human multiple tumour suppression protein,
CC MTS1. The MTS gene locus is also referred to as the familial melanoma
CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations
CC in MTS genes can be used in the diagnosis of predisposition to cancers,
CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
CC ovary, uterus, testis, kidney, stomach and rectum.
XX
XX Sequence 156 AA:
SQ
Query Match 81.8%; Score 121; DB 19; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 ALPNAPNSYGRPIQVMMGSAFYAEILLHGAEPCADPATLTRPVHDAAREGFIDTLV 87
DB 36 alpnapnsygrripqymmgasrvaellllhgaeppcadpatltrpvhdaaregfldtlv 95
QY 88 VLHRAGARLDVDRDAMGRPLVDLAEEIGHRDVARYLRAAAGTSGSNHARIDAAGPSDIP 147
DB 96 vlhragarldvdrdawgrlpvdlaeelghrdvarylraaagtrsgsnharidaaegpsdip 155
QY 148 P 148
DB 156 d 156
RESULT 16
AAW80524
ID AAW80524 standard; Protein; 156 AA.
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XX AC AAW80524;
XX DT 03-FEB-1999 (first entry)
XX DE A human multiple tumour suppressor 1 (MTS1) protein.
XX KW Human; multiple tumour suppressor 1 gene; MTS1; cancer.
XX OS Homo sapiens.
XX PN US5843756-A.
XX PD 01-DEC-1998.
XX PF 28-JUL-1995; 95WO-0508735.
XX PR 28-JUL-1995; 95US-0508735.
XX PR 07-JUN-1995; 95US-0487033.
XX (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
XX WPI: 1999-044585/04.
XX DR N-PSDB; AAV70583.
XX PT Mouse multiple tumour suppressor gene segment - useful for primer
XX design
XX PS Disclosure; Columns 65-66; 80pp; English.
XX CC The present sequence represents a human multiple tumour suppressor 1
XX CC (MTS1) protein. The sequence is homologous to the corresponding
XX CC murine gene. Primers designed from the gene can be used to design
XX CC primers to detect abnormalities i.e. polymorphisms which may
XX CC predispose towards malignancies such as melanoma, leukaemia,
XX CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
XX CC thyroid, pancreas, uterus and kidneys.
XX SQ Sequence 156 AA;

Query Match 81.8%; Score 121; DB 20; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAANSYGRRIQVMMGSAKYAEELLHGAEPNCADPATLTTRPVHDAAREGFLDTLV 87
DB 36 alpnapnsygrripqymmmgsarvaeelllhgaepncadpatlttrpvhdaaregfldtlv 95
QY 88 VLHRAGARLDVDRDAMGRLPVDLAEEIGHRDVARYLRAAGTGRGNSNHARIDAEGPSDIP 147
DB 96 vlhragarldvdrdavgrlpvdlaeeighrdvarylraaagtrgnsnharidaaegpsdip 155
QY 148 D 148
DB 156 d 156

RESULT 17
AAB15498
ID AAB15498 standard; Protein; 156 AA.
XX
AC AAB15498;
XX
XX 14-FEB-2001 (first entry)
XX DT
XX DE Human MTS1 protein.
XX KW Cytostatic; human; multiple tumour suppressor 1; MTS1; diagnostic;
XX KW cancer; gene therapy; protein replacement therapy.
XX

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OS Homo sapiens.
XX US6090578-A.
XX PN 18-JUL-2000.
XX PD 08-DEC-1997; 97US-0986515.
XX PF 07-JUN-1995; 95US-0480810.
XX PR 18-MAR-1994; 94US-0214582.
XX PR 18-MAR-1994; 94US-0215086.
XX PR 18-MAR-1994; 94US-0215087.
XX PR 14-APR-1994; 94US-0227369.
XX PR 01-JUN-1994; 94US-0251938.
XX PR 17-MAR-1995; 95WO-US03316.
XX (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
XX WPI: 2000-514036/46.
XX DR N-PSDB; AAA95633.
XX PT Novel protein composition useful in protein replacement therapy for
XX PT diagnosing and treating cancer comprises a specific weight percent of
XX PT human multiple tumour suppressor 1 polypeptide -
XX PS Claim 4; Column 63-64; 72pp; English.
XX CC This sequence represents the human multiple tumour suppressor 1 (MTS1) in
XX CC amino acid sequence. The protein has a cytosolic activity and is used in
XX CC protein replacement therapy. MTS1 is useful in diagnosing human cancers
XX CC such as (ocular) melanoma, leukemia, astrocytoma, glioblastoma, lymphoma,
XX CC glioma, Hodgkin's lymphoma, multiple myeloma, sarcoma, myosarcoma,
XX CC cholangiocarcinoma, squamous cell carcinoma, CLL, and cancers of
XX CC pancreas, breast, stomach, brain, prostate, bladder, thyroid, ovary,
XX CC uterus, testis, kidney, colon and rectum. The MTS1 gene and protein is
XX CC useful in gene therapy, protein replacement therapy and protein mimetic
XX CC studies.
XX SQ Sequence 156 AA;

Query Match 81.8%; Score 121; DB 21; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAANSYGRRIQVMMGSAKYAEELLHGAEPNCADPATLTTRPVHDAAREGFLDTLV 87
DB 36 alpnapnsygrripqymmmgsarvaeelllhgaepncadpatlttrpvhdaaregfldtlv 95
QY 88 VLHRAGARLDVDRDAMGRLPVDLAEEIGHRDVARYLRAAGTGRGNSNHARIDAEGPSDIP 147
DB 96 vlhragarldvdrdavgrlpvdlaeeighrdvarylraaagtrgnsnharidaaegpsdip 155
QY 148 D 148
DB 156 d 156

RESULT 18
AAV97524
ID AAV97524 standard; Protein; 156 AA.
XX
AC AAV97524;
XX
XX 15-JAN-2001 (first entry)
XX DT
XX DE Human p16 protein sequence.
XX KW Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;
XX KW adenovirus E4 protein; neoplasia; p16 protein.
XX

```

Query Match	81.8%; Score 121; DB 21; Length 156;
Best Local Similarity	100.0%; Pred. No. 1.e-108;
Matches 121; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY 28	ALPAPASVRRRIQYMMGSAVAVELLILHGAEPCNDPATLTPRVHDAAREGFLDTLV 87
DB 36	alpnapsygrpdyvmmggsarvae11llllygaepncadpatlltrpvdaaregfldtlv 95
QY 88	VLNAGARLQVPRAMQRLPVDLAEEIGHRDVARYRAAAGCTRGCSNHRIDDAEGSPDIP 147
DB 96	vlhagargldvrdawgrlpvdiacelghdvarylraaagtlrgsnhridaaegspdp 155
QY 148	D 148
DB 156	d 156
RESULT 19	
AAI96053	
ID	AAI96053 standard; Protein; 156 AA.
XX	
AC	AAI96053;
XX	
DT	05-DEC-2000 (first entry)
XX	
DE	Human cyclin dependent kinase inhibitor p16.
XX	
KW	Cyclin dependent kinase inhibitor; CDK1; INK4; human; p16;
XX	
KW	smooth muscle cell; restenosis; vasotropic; antiproliferative;
XX	
OS	Homo sapiens.
XX	
PN	MO200052159-A1.

XX 08-SEP-2000.  
PD  
XX  
XX 28-FEB-2000; 2000OWO-US04971.  
PF  
XX  
XX 01-MAR-1999; 99US-0122974.  
PR 05-NOV-1999; 99US-0163682.  
PR 09-DEC-1999; 99US-0457568.  
XX  
XX (CELL-) CELL GENESYS INC.  
PA (MITO-) MITOFTX INC.  
PI McArthur J, Gyuris J, Finer M;  
XX  
DR WPI: 2000-594183/56.  
DR N-PDB: AAA50500.

PT Novel recombinant lentivirus for inhibiting proliferation of smooth  
PT muscle cells in e.g. restenosis, is replication deficient and comprises  
PT a transgene encoding a cyclin dependent kinase inhibitor -  
XX  
XX  
PS Example 1; Page 121; 126pp; English.

The present sequence is that of human p16, a cyclin dependent  
CC kinase inhibitor (CDK1) that inhibits smooth muscle cell  
CC proliferation. A claimed method for inhibiting smooth muscle cell  
CC hyperproliferation involves transducing smooth muscle cells with a  
CC replication-deficient recombinant adenovirus that lacks a functional  
CC E1 region and a functional E4 region, and comprises a transgene  
CC encoding a CDK1. The CDK1 is selected from an INK4 family protein  
CC such as human p16, a CIP/KIP family protein such as p27, active  
CC fragments of these, or fusion proteins comprising (active fragments  
CC of) an INK4 family protein and a CIP/KIP family protein (see AA96046  
CC and AA96049). The method is used to inhibit mammalian smooth muscle  
CC cell hyperproliferation induced by injury caused by angioplasty,  
CC stent placement or vein engraftment. It is useful for treating  
CC vascular pathologies, e.g. restenosis. Also claimed are recombinant  
CC lentiviruses encoding CDKis.

SQ Sequence 156 AA:

```

      81.8%; Score 121; DB 21; Length 156;
Query Match Best Local Similarity 100.0%; Pred. No. 1,6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	28	ALPNAPNSYGRBPPIOVMNGSARVAELLHGAEPNCADPATLTFRPHDAAREGLDTLV	87
DB	36	alpnapnsygrbpriqymngsarvaeelllhgaepncadpatltfrphdaaregfditlv	95
QY	88	VLMRRGARLDVDNMCRLPVDLAEELGHDVARYRAAAGCRGSNMHRIDAEGPSPDTP	147
DB	96	vlmrgarldvdnmcrlpvdlaeelghdvarylraaagcrgsnmhridaegpsdp	155
QY	148 D	148	
DB	156 d	156	

RESULT 20  
AA96067  
ID AA96067 standard; Protein; 156 AA.  
XX  
XX  
AC AA96067;  
XX  
DT 05-DEC-2000 (first entry)  
XX  
DE Human cyclin dependent kinase inhibitor p16.  
XX  
XX Cyclin dependent kinase inhibitor; CDK1; INK4; human; p16;  
KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
KW antiangiogenic; psoriasis; vascular retinopathy; cytostatic;  
KW antidiabetic; antineumatic; gynaecological; antiproliferative;

PT Inhibiting angiogenesis and treating angiogenesis-associated  
PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
PT cell with a recombinant virus having a transgene encoding a cyclin  
PT dependent kinase inhibitor -  
XX  
PS Example 1; Page 129; 138pp; English.

CC The present sequence is that of human p16, a cyclin dependent  
CC kinase inhibitor (CDKI) that inhibits angiogenesis. A claimed  
CC method for inhibiting angiogenesis involves transducing an  
CC epithelial cell with a transgene encoding (internally, or  
CC secretably) CDKI. The delivery system for the transgene may be a  
CC liposome or a recombinant virus. The CDKI is preferably a protein  
CC of the CIP/KIP family such as p27, a protein of the INK4 family  
CC such as p16, active fragments of these proteins, or a fusion of 2  
CC CDKI proteins such as p27 and p16 (see AY96068-80). The method is  
CC useful in treating conditions associated with angiogenesis, e.g.  
CC neoplasia, rheumatoid arthritis, endometriosis, psoriasis and  
CC vascular retinopathy (claimed). Alternatively, the transgene is  
CC delivered to an auxiliary cell, and is expressed by that cell such  
CC that the CDKI is released into the blood and contacts the target  
CC epithelial cell.

	Query Match	Similarity	81.88%	Score 121	DB 21	Length 156
Db	28	ALPNAENSGRRPIQVMKMSARVAELLHLHGAEPCADPATLTRPYDAAREGFLDTLV	100.00%	Pred. No. 1.6e-108	0	Indels 0; Caps 0
Db	36	alpnepnsgrrpdlqymmgasrvaelllllhgepcadpalltrpydaaregfltlv	95			
QY	88	VLHRGARDLVVDAMGRLLPVDLAEELGHRDVAEYLLAAAGCGTSNHRIRIAAGPSDIP	147			
Db	96	vlhragarldvrdagrrlpvdlaelghrdvatylraaagcgtrgsnharltaaagpsdip	155			
QY	148	D 148				
Db	156	d 156				

RESULT	21
AAV92921	
ID	AAV92921 standard; Protein; 156 AA.
XX	
AC	AAV92921;
XX	
DT	11-OCT-2000 (first entry)
XX	

DE	Human multiple tumour suppressor 1 protein.
XX	
XX	Variant; human; multiple tumour suppressor; MTS; mutation; melanoma
KW	cancer; diagnosis.
XX	
OS	Homo sapiens.
XX	
PN	US6037462-A.
PD	
PD	14-MAR-2000.
XX	
PE	22-JUL-1998; 98US-0120130.
XX	
PR	07-JUN-1995; 95US-0480810.
PR	18-MAR-1994; 94US-0214582.
PR	18-MAR-1994; 94US-0215086.
PR	18-MAR-1994; 94US-0215087.
PR	14-APR-1994; 94US-0227369.
PR	01-JUN-1994; 94US-0251938.
PR	17-MAR-1995; 95WO-US03316.
XX	
PA	(MYRI-) MYRIAD GENETICS INC.
XX	
PI	Kamb A;
XX	
WPI	2000-269915/23.
DR	N-PSDB; AAA11165.
DR	

PT	New mutants of the human multiple tumor suppressor gene, useful as
PT	diagnostic markers of cancer, contain specific base alterations or
PT	deletions -
XX	
PS	Disclosure; Column 61-62; 72pp; English.
XX	
CC	The invention relates to variants (AA11196-A11206) of the human
CC	multiple tumour suppressor 1 (MSI1) protein of which this sequence
CC	represents the wild type sequence. The variants have the following
CC	changes relative to the wild type coding sequence: A at any of positions
CC	263, 442, 330 and 329; T at any of positions 172, 238, 341 and 148 and
CC	deletions of nucleotides 290-294, 172-179 or 128-129. The variants are
CC	dominant mutations of MSI1, indicative of predisposition to melanoma and
CC	many other cancers, so detecting them is useful for diagnosis, prognosis
CC	and monitoring of cancer (including prenatal analysis). Cells and
CC	animals that express the variants are useful as model systems for
CC	identifying potential anticancer agents.
XX	
XX	
Sequence	156 AA;

Query Match	81.8%	Score 121	DB 21	Length 156
Best Local Similarity	100.0%	Pred. 1.6e-108		
Matches 121	Conservative	0	Mismatches 0	Indels 0
				Gaps 0
QY	28	ALNAPNSYGRPIQVMMGARSVAE	LLLLGAEPCNADPATLRPVHDAA	REGFLDTLY 87
Db	36	alnapsygrripqymmgarsvae	lllllgaepncdpatlrrpvhdaa	regfldtly 95
QY	88	VLRAGARLDVDRDAMGRLPVDLAE	LIGHRDYARYLRAAGSTRGNSNR	ARIDAAEGSPDIP 147
Db	96	vlnragarldvdrdagrllpvdlae	lghrdrvarylraaagstrgnsn	aridaaegspdlp 155
QY	148	D 148		
Db	156	d 156		

RESULT	22
AA91102	
ID	AA91102 standard; Protein; 156 AA.
XX	
AC	AA91102;
XX	
DT	12-SEP-2000 (first entry)

```

XX DE Human multiple tumour suppressor MTS1 SEQ ID NO:2.
XX XX
XX KW Human; multiple tumour suppressor; MTS; somatic mutation; cancer;
XX KW diagnosis; germ line mutation; gene therapy; cytostatic; melanoma;
XX KW leukemia; astrocytoma; glioblastoma; lymphoma; glioma;
XX KW Hodgkin's lymphoma.
XX XX
XX OS Homo sapiens.
XX XX
XX PN US6060301-A.
XX XX
XX PD 09-MAY-2000.
XX XX
XX PF 14-JUL-1998; 98US-0115252.
XX XX
XX PR 07-JUN-1995; 95US-0480810.
XX PR 08-DEC-1997; 97US-0986147.
XX PR 18-MAR-1994; 94US-0214582.
XX PR 18-MAR-1994; 94US-0215086.
XX PR 18-MAR-1994; 94US-0215087.
XX PR 14-APR-1994; 94US-0227369.
XX PR 01-JUN-1994; 94US-0251938.
XX PR 17-MAR-1995; 95WO-0503316.
XX XX
XX PA (MYRI-) MYRIAD GENETICS INC.
XX PI
XX PI Kamb A;
XX XX
XX XX WPI; 2000-349676/30.
XX DR N-PSDB; AAA39353.
XX XX
XX PT New vector useful for gene therapy of cancer associated with mutation
XX PT in tumor suppressor gene, comprises DNA sequence of multiple tumor
XX PT suppressor gene.
XX XX
XX PS Disclosure; Column 63-64; 71pp; English.
XX XX
XX CC The present invention describes a vector (I) comprising an isolated DNA
XX CC sequence of a multiple tumour suppressor (MTS) gene having a
XX CC polynucleotide sequence of the human MTS1E1-beta. (I) is useful for
XX CC introducing wild-type MTS function to a cancerous or pre-cancerous cell
XX CC which carries diminished or mutant MTS alleles for suppressing
XX CC neoplastic growth of the recipient cells. (I) is also useful for
XX CC increasing the level of expression of MTS gene even in tumour cells in
XX CC which the mutant gene is expressed at a normal level but the gene
XX CC product is not fully functional. A host cell transformed with (I) is
XX CC useful as a model system to study cancer remission and drug treatment
XX CC which promotes such remission. The present invention relates to somatic
XX CC mutations and germ line mutations in the MTS gene and their use in the
XX CC diagnosis and prognosis of human cancer e.g. melanoma, leukaemia,
XX CC astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, and
XX CC cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney,
XX CC stomach and rectum. The present sequence represents human MTS1, which is
XX CC used in the exemplification of the present invention.
XX XX
XX SQ Sequence 156 AA:

```

```

Query Match 81.8%; Score 121; DB 21; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 28 ALPNAPNSYGRPIQVMMGSAKVAELLLHGAEPCADPATLTRPVHDAAREGFLDTLV 87
DB 36 alpnapnsygrripqymmgasrvaellllhgaeppcadpatltrpvhdaaregfldtlv 95
QY 88 VLHRAGARLDVBDAMGRPLVPDLAEELGHRDVARYLRAAAGTRGSNHRIRDAEESPSP 147
DB 96 vlnrgarldvbdawgrlplvpdlaeelghrdvarylraaagtrgsnhrirdaaespdp 155
QY 148 P 148

```

```

DB 156 d 156
RESULT 23
AAVS9415
ID AAVS9415 standard; Protein: 156 AA.
XX
XX AC AAVS9415;
XX XX
XX DT 21-MAR-2000 (first entry)
XX XX
XX DE Human MTS1 protein sequence.
XX XX
XX KW MTS; human; polymorphism detection; cancer predisposition; astrocytoma;
XX KW Multiple Tumour Suppressor gene; melanoma; leukaemia; glioblastoma;
XX KW lymphoma; glioma; Hodgkin's lymphoma; chronic lymphocytic leukaemia;
XX KW therapy; MTS1.
XX XX
XX OS Homo sapiens.
XX XX
XX PN US5989815-A.
XX XX
XX PD 23-NOV-1999.
XX XX
XX PF 29-APR-1997; 97US-0848251.
XX XX
XX PR 07-JUN-1995; 95US-0474083.
XX PR 18-MAR-1994; 94US-0214582.
XX PR 18-MAR-1994; 94US-0215086.
XX PR 18-MAR-1994; 94US-0215087.
XX PR 14-APR-1994; 94US-0227369.
XX PR 01-JUN-1994; 94US-0251938.
XX PR 17-MAR-1995; 95WO-0503357.
XX XX
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PA (MYRI-) MYRIAD GENETICS INC.
XX PI
XX PI Skolnick MH, Cannon-Albright LA, Kamb A;
XX XX
XX XX WPI; 2000-070785/06.
XX DR N-PSDB; AAZ48770.
XX XX
XX PT Diagnosing a polymorphism associated with a predisposition for cancer -
XX PT Claim 1; Column 61-64; 74pp; English.
XX PS
XX XX This sequence represents the human MTS1 protein.
XX CC The invention relates to a method for diagnosing a polymorphism
XX CC associated with a predisposition to cancer by detecting a germ-line
XX CC alteration of a wild-type Multiple Tumour Suppressor (MTS) gene or its
XX CC expression products in a human sample. The method comprises detecting a
XX CC germ-line alteration of a wild-type MTS gene or its expression products
XX CC in a human sample, the alteration indicating a predisposition to at least
XX CC one of the cancers. The cancer is selected from melanoma, leukaemia,
XX CC astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma,
XX CC chronic lymphocytic leukaemia (CLL), and cancers of the pancreas, breast,
XX CC thyroid, ovary, uterus, testis, kidney, stomach and rectum. The method
XX CC may be used as the basis for developing very important diagnostic tests
XX CC capable of predicting the predisposition to cancer. The MTS gene is
XX CC involved in the progression of multiple tumour types and may provide
XX CC means for a general anti-cancer therapy by virtue of its ability to
XX CC suppress tumour growth.
XX XX
XX SQ Sequence 156 AA:

```

```

Query Match 81.8%; Score 121; DB 21; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 28 ALPNAPNSYGRPIQVMMGSAKVAELLLHGAEPCADPATLTRPVHDAAREGFLDTLV 87
DB 36 alpnapnsygrripqymmgasrvaellllhgaeppcadpatltrpvhdaaregfldtlv 95

```

OY 88 VLRAGARLDVDRDAMGRLPVDLAEEIGHRDVARYLRAAAGCTGSGNHARIDAEGPSDIP 147  
 |||||||  
 Db 96 vlhragarldvdrdawgripvdlaeelghrdvarylraaagctrgsnharidaaegpsdip 155  
 OY 148 D 148  
 |  
 Db 156 d 156

## RESULT 24

AAV54902

ID AAV54902 standard; Protein: 156 AA.

XX AAV54902;

XX 11-FEB-2000 (first entry)

XX Human multiple tumour suppressor 1 protein sequence.

XX Multiple tumour suppressor: MTS2; human; diagnosis; Hodgkin's lymphoma;  
 cancer predisposition; melanoma; leukaemia; lymphoma; glioma; MTS1.

XX Homo sapiens.

XX US5994095-A.

XX 30-NOV-1999.

XX 07-JUN-1995; 95US-0486047.

XX 18-MAR-1994; 94US-0214582.

XX 18-MAR-1994; 94US-0215086.

XX 18-MAR-1994; 94US-0215087.

XX 14-APR-1994; 94US-0227369.

XX 01-JUN-1994; 94US-0251938.

XX 17-MAR-1995; 95WO-US03316.

XX (MYRI-) MYRIAD GENETICS INC.

XX Kamb A;

XX WPI: 2000-038259/03.

XX N-PSDB: AA239974.

XX Multiple tumour suppressor cDNA, useful for diagnosing or determining a

XX predisposition to cancer -

XX Disclosure: Column 61-62; 72pp; English.

XX This sequence represents the human multiple tumour suppressor 1 (MTS1)

XX protein. The invention relates to the human MTS2 DNA and protein

XX sequences. The DNA sequences are useful for diagnosing or determining a

XX predisposition to cancers e.g. melanoma, leukaemia, lymphoma, glioma,

XX Hodgkin's lymphoma and cancers of the pancreas, breast, thyroid, ovary,

XX kidney, uterus and stomach.

XX Sequence 156 AA;

XX

OY 148 D 148

Db 156 d 156  
 |

## RESULT 25

AAU02122

ID AAU02122 standard; Protein: 156 AA.

XX AAU02122;

XX 29-AUG-2001 (first entry)

XX Human multiple tumour suppressor MTS1, amino acid sequence.

XX Human: multiple tumour suppressor: MTS1; MTS2; therapeutic; diagnostic;  
 cancer; gene therapy; melanoma; leukaemia; astrocytoma; glioblastoma;

XX Lymphoma; glioma; Hodgkin's lymphoma; chronic lymphatic leukaemia.

XX Homo sapiens.

XX US6210949-B1.

XX 03-APR-2001.

XX 30-NOV-1998; 98US-0201139.

XX 28-JUL-1995; 95US-0508735.

XX 17-MAR-1995; 95WO-US03316.

XX 07-JUN-1995; 95US-0487033.

XX (MYRI-) MYRIAD GENETICS INC.

XX Stone S, Jiang P, Kamb A;

XX WPI: 2001-280859/29.

XX N-PSDB: AAS02564.

XX New mouse multiple tumour suppressor gene, useful for diagnosing or

XX prognosing human cancer or as gene therapy for treating cancer,

XX particularly melanoma, leukemia, astrocytoma, lymphoma or cancers of

XX the pancreas or breast -

XX Disclosure: Fig 19; 80pp; English.

XX The sequence represents the amino acid sequence of human multiple tumour

XX suppressor MTS1. The MTS genes, and expression products, are useful for

XX treating, diagnosing or prognosing human cancer. In particular, the MTS

XX gene is useful for diagnosing a predisposition to or as a gene therapy

XX for melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,

XX Hodgkin's lymphoma, chronic lymphatic leukaemia (CLL), or cancers of the

XX pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach or

XX rectum. The gene may be used in both cancerous and pre-cancerous cells.

XX Sequence 156 AA;

XX

OY 28 ALPNAPNSYGRPIQVMMGSAKYAEILLHGAEPNCADPATITRPHVDAAREGFLDTLY 87

Db 36 alpnapnsygrpiqvmmsarvaeilllghaepncadpatlirphdaaregfltdlty 95

OY 88 VLRAGARLDVDRDAMGRLPVDLAEEIGHRDVARYLRAAAGCTGSGNHARIDAEGPSDIP 147

Db 96 vlhragarldvdrdawgripvdlaeelghrdvarylraaagctrgsnharidaaegpsdip 155

OY 148 D 148

Db 156 d 156

```

RESULT 26
AAE01002
ID AAE01002 standard; Protein: 156 AA.
AC
XX
XX AAE01002;
XX
XX 04-JUL-2001 (first entry)
XX
XX Human multiple tumor suppressor 1 (MTS1) protein.
XX
XX Human; multiple tumor suppressor; MTS1; cytosolic; somatic mutation;
XX germ line mutation; gene therapy; melanoma; leukaemia; astrocytoma; CLL;
XX glioblastoma; lymphoma; glioma; Hodgkin's lymphoma; cancer; rectum;
XX pancreas; breast; thyroid; ovary; uterus; testis; kidney; stomach;
XX chromosome 9p21.
XX
XX Homo sapiens.
XX
XX OS
XX US6218146-B1.
XX
XX 17-APR-2001.
XX
XX 22-JUL-1998; 98US-0120131.
XX
XX 07-JUN-1995; 95US-0486047.
XX 18-MAR-1994; 94US-0214582.
XX 18-MAR-1994; 94US-0215086.
XX 18-MAR-1994; 94US-0215087.
XX 14-APR-1994; 94US-0227369.
XX 01-JUN-1994; 94US-0251938.
XX 17-MAR-1995; 95WO-0503316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Kamb A;
XX
XX WPI: 2001-289831/30.
XX N-PSDB; AAD04692, AAD04693, AAD04694, AAD04724, AAD04727, AAD04734,
XX AAD04735.
XX
XX Novel multiple tumor suppressor proteins useful for diagnosis and
XX prognosis of human cancer and for screening drugs for cancer treatment
XX
XX
XX Example 9; Column 63-64; 71pp; English.
XX
XX The invention relates to somatic and germ line mutations in the
XX multiple tumor suppressor (MTS) gene in human cancer. The invention
XX also relates to therapy of human cancer which have a mutation in the
XX MTS gene, including gene therapy, protein replacement therapy, and
XX protein mimetics. The MTS sequences are useful for diagnosing
XX predisposition to human cancer or for diagnosing and prognosing
XX human cancers such as melanoma, leukaemia, astrocytoma, glioblastoma,
XX lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of pancreas,
XX breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
XX They are also used for screening drugs for cancer treatment.
XX The present sequence is human MTS1 protein which is encoded on
XX chromosome 9p21.
XX
XX Sequence 156 AA;

```

```

Query Match 81.8%; Score 121; DB 22; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 28 ALPNAPNSYGRPIQVMMGSAKYAEILLHGAEPCADPATLTRPVHDAAREGFLDTLY 87
DB 36 alpnapnsygrripqymmgasayaeellllhgaepncadpatltrpvhaaregfltdlty 95
OY 88 VLHRAGARLDVDAWGRLPVDLAEEELGHRDVARYLRAAAGTSGSHARIDAEGPSDIP 147
DB 96 vlhragarldvrdawgrlpvdlaeelghrdvarylraaagtgsgsharidaegpsdip 155

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```

RESULT 27
AAB67334
ID AAB67334 standard; protein: 156 AA.
AC
XX
XX AAB67334;
XX
XX 23-APR-2001 (first entry)
XX
XX Protein encoded by multiple tumour suppressor open reading frame #2.
XX
XX
XX Human; multiple tumour suppressor; MTS; cancer; gene therapy.
XX
XX OS
XX Homo sapiens.
XX
XX OS
XX US6180776-B1.
XX
XX 30-JAN-2001.
XX
XX 22-JUL-1998; 98US-0120129.
XX
XX 07-JUN-1995; 95US-0486047.
XX 18-MAR-1994; 94US-0214582.
XX 18-MAR-1994; 94US-0215086.
XX 18-MAR-1994; 94US-0215087.
XX 01-JUN-1994; 94US-0251938.
XX 17-MAR-1995; 95WO-0503316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Kamb A;
XX
XX WPI: 2001-158668/16.
XX
XX Novel multiple tumor suppressor gene useful for diagnosing, prognosing
XX and treating cancers, such as melanoma, leukemia, glioblastoma and
XX Hodgkin's lymphoma -
XX
XX Disclosure; Column 63; 71pp; English.
XX
XX The present invention relates to human multiple tumor suppressor-2
XX (MTS2) gene. The invention is useful for diagnosing, prognosing and
XX treating cancers. It is also useful for screening drugs for cancer
XX therapy and gene therapy.
XX
XX Sequence 156 AA;

```

```

XX AAB36890;
AC
XX 23-FEB-2001 (first entry)
DT
XX Human Multiple Tumour Suppressor 1 protein.
DE
XX MTS; Multiple Tumour Suppressor; cancer; antibody.
XX Homo sapiens.
XX US6140473-A.
XX 31-OCT-2000.
XX 22-JUL-1998; 98US-0120128.
XX
XX 07-JUN-1995; 95US-0486047.
XX 18-MAR-1994; 94US-0214582.
XX 18-MAR-1994; 94US-0215086.
XX 18-MAR-1994; 94US-0215087.
XX 14-APR-1994; 94US-0227369.
XX 01-JUN-1994; 94US-0251938.
XX 17-MAR-1995; 95WO-US03316.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX Kamb A;
XX WPI; 2001-014867/02.
XX N-PSDB; AAC83071.
XX
XX New multiple tumor suppressor 2-specific antibodies useful for
XX detecting differences in the absence of the peptides or mutant gene
XX products, or for screening tissues -
XX
XX Claim 1; Column 63; 71pp; English.
XX
XX The present invention relates to an antibody or its fragment that
XX specifically binds to a human multiple tumour suppressor (MTS). The
XX invention is useful for detecting differences in the absence of MTS
XX peptides, to screen a tissue or to detect mutant MTS gene products.
XX The antibodies will immunoprecipitate MTS proteins from solution as
XX well as react with MTS protein on Western or Immunoblots of
XX polyacrylamide gels.
XX
XX Sequence 156 AA;
SQ
Query Match 81.8%; Score 121; DB 22; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 ALPNAPNSYGRPIQVMMGSAARVAEILLHGAEPCADPATLTPRVHDAAREGFLDTLV 87
DB 36 alpnapnsygrripqymmmgsarvaeilllhgaepncadpatltprvhdaaregfldtlv 95
QY 88 VLHRAGARLDVNDAMGRPLVDAELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147
DB 96 vlhragarldvndamgrplvdaelaehgrdvarylraaagtrsgsnharidaegpsdip 155
QY 148 D 148
DB 156 d 156
RESULT 29
AA97522
ID AA97522 standard; Protein; 228 AA.
AC
XX AA97522;
XX
XX 15-JAN-2001 (first entry)
DT

```

```

XX Human W9 protein sequence.
DE
XX Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;
XX adenovirus E4 protein; neoplasia; W9 protein.
XX
XX Homo sapiens.
XX WO200052184-A1.
XX
XX 08-SEP-2000.
XX
XX 01-MAR-2000; 2000WO-US05350.
XX
XX 01-MAR-1999; 99US-0122974.
XX 08-APR-1999; 99US-0128271.
XX 09-APR-1999; 99US-0128515.
XX
XX (CELL-) CELL GENESYS INC.
XX (MITO-) MITOTIX INC.
XX
XX Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;
XX
XX WPI; 2000-587315/55.
XX N-PSDB; AAA90919.
XX
XX Protein and nucleic acid compositions for preventing and treating
XX neoplasias (particularly cancer), comprises a novel chimeric cyclin
XX dependent kinase inhibitor and adenovirus E4 protein -
XX
XX Example 1; Fig 2b; 126pp; English.
XX
XX This sequence represents the human W9 protein.
XX The invention relates to a protein composition comprising a novel
XX purified chimeric cyclin dependent kinase inhibitor (CDK1) and a
XX or the DNA encoding it are useful for treating neoplasias in animals. The
XX compositions also find use in assays to eliminate a specific
XX subpopulation of cultured cells, to determine the susceptibility of
XX neoplastic cells to treatment with the compositions and also in assays to
XX synchronise cell growth in cultured cells.
XX
XX Sequence 228 AA;
SQ
Query Match 81.8%; Score 121; DB 21; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.2e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 ALPNAPNSYGRPIQVMMGSAARVAEILLHGAEPCADPATLTPRVHDAAREGFLDTLV 87
DB 108 alpnapnsygrripqymmmgsarvaeilllhgaepncadpatltprvhdaaregfldtlv 167
QY 88 VLHRAGARLDVNDAMGRPLVDAELGHRDVARYLRAAAGTSGSNHARIDAEGPSDIP 147
DB 168 vlhragarldvndamgrplvdaelaehgrdvarylraaagtrsgsnharidaegpsdip 227
QY 148 D 148
DB 228 d 228
RESULT 30
AA96051
ID AA96051 standard; Protein; 228 AA.
AC
XX AA96051;
XX
XX 05-DEC-2000 (first entry)
DT
XX Antiproliferative truncated p27-p16 fusion protein W9.
XX
XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;
KW

```



KW p16; human; smooth muscle cell; hyperproliferation; restenosis;  
KW vasotrophic; antiproliferative; gene therapy; mutant; mutein.  
OS Homo sapiens.  
XX Synthetic.

	Key	Location/Qualifiers
FT	Protein	1..71
FT		/label= p27(25-93)
FT		84..228
FT	Protein	/label= p16

MOZ00052159-A1.  
XX PD  
XX PD 08-SEP-2000.  
XX PF 28-FEB-2000; 2000WO-US04971.  
XX PR 01-MAR-1999; 99US-0122974.  
XX PR 05-NOV-1999; 99US-0163682.  
XX PR 09-DEC-1999; 99US-0457568.  
PA (CELL-) CELL GENESYS INC.  
PI (MITO-) MITOTIX INC.  
PI McArthur J, Gyuris J, Finer M;  
XX WPI: 2000-594183/56.  
DR N-PSDB: AAA50498.  
XX PT Novel recombinant lentivirus for inhibiting proliferation of smooth  
PT muscle cells in e.g. restenosis, is replication deficient and comprises  
PT a transgene encoding a cyclin dependent kinase inhibitor -  
XX PS Example 1; Page 118-119; 126pp; English.

The present sequence is that of W9 fusion protein comprising a truncated human p27 protein (see AAY96048) in which only the cyclin dependent kinase inhibitor (CDK1) domain is retained, and human p16 protein (see AA996053), with no (GLY4Ser)3 hinge. A claimed method for inhibiting smooth muscle cell hyperproliferation involves transducing smooth muscle cells with a replication-deficient recombinant adenovirus that lacks functional E1 and E4 regions, and comprises a transgene encoding a CDK1. The CDK1 is selected from an INK4 family protein such as human p16, a CIP/KIP family protein such as p27, active fragments of these, or fusion proteins comprising (active fragments of) an INK4 family protein and a CIP/KIP family protein (see AAY96046 and AAY96049). A fusion protein comprising W9 is specifically claimed. The method is used to inhibit mammalian smooth muscle cell hyperproliferation induced by injury caused by angioplasty, stent placement or vein engraftment. It is useful for treating vascular pathologies e.g., restenosis. Also claimed are recombinant lentiviruses encoding CDKis. Use of truncated p27 was designed to increase the protein's half-life and to eliminate potential phosphorylation sites involved in the negative regulation of CDK1 activity. The p27-p16 fusion proteins interact with the CDK4/cyclinD, CDK2/cyclina and CDK2/cycline complexes and inhibit cell cycle progression at multiple points.

Sequence 228 AA:

```

Query Match          81.8%; Score 121; DB 21; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.2e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

28 ALPNAENSYGRPIIVMMGARSARELLLHGAEPNCADPATLRPVHDAREGFIDTLV 87  
|||||  
db 108 alapnapnsygrripdyvmmgasrarel||lllhgaepncadpatltprvydaaregfidtlv 167  
|||||  
QY VILRRGARLDVDAMGRLPVLDLAELGHBDVARYLRAAAGTRGSNHRIDAEGPSDIP 147  
|||||

D6	168	vlnrgrarldvrdwgrlpvdlaeelghrcdrvarylraagsgtgsnharidaegpsdip	27
Oy	148 D	148	
D6	228 d	228	
 RESULT 31			
AAI96078	ID	AAI96078 standard; Protein; 228 AA.	
XX	AC	AAI96078;	
XX	DT	05-DEC-2000 (first entry)	
DE	XX	Angiogenesis inhibitor p27(25-93)-p16 fusion W9.	
XX	KW	Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; human; p27;	
KW	KM	angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;	
KW	KM	endometriosis; psoriasis; vascular retinopathy; cystostatic;	
KW	KM	antiarthritic; antihumetic; gynaecological; antipsoriatic;	
KW	KM	antiproliferative; gene therapy; mutant; mutein.	
OS	XX	Homo sapiens.	
OS	XX	Synthetic.	
XX	FH	Key	Location/Qualifiers
FT	FT	/label= p27(25-93)	1..71
FT	FT	Protein	84..228
FT	FT		/label= p16
PN	XX	WO200052158-A1.	
PD	XX	08-SEP-2000.	
PR	XX	26-FEB-2000; 2000MO-US04970.	
XX	XX		
PR	XX	01-MAR-1999; 99US-0122974.	
PR	XX	05-NOV-1999; 99US-0163682.	
PR	XX	09-DEC-1999; 99US-0457646.	
PA	XX	(CELL-) CELL GENESYS INC.	
PA	XX	(MITO-) MITOTIX INC.	
P1	XX	Patel S, McArthur J, Gyuris J;	
DR	XX	WPI: 2000-565501/52.	
DR	XX	N-PSDB; AAA50533.	
PT	XX	Inhibiting angiogenesis and treating angiogenesis-associated	
PT	XX	conditions, e.g. neoplasia, psoriasis by transducing an endothelial	
PT	XX	cell with a recombinant virus having a transgene encoding a cyclin	
PT	XX	dependent kinase inhibitor -	
PS	XX	Example 1; Page 126-127; 138pp; English.	
CC	XX	The present sequence is that of fusion protein W9 comprising an	
CC	XX	N-terminal truncated human p27 protein (see AAI96075) in which only	
CC	XX	the cell dependent kinase inhibitory (CDK1) domain was retained,	
CC	XX	and a human p16 protein (see AAI96067). This version of W9 differs	
CC	XX	from that of AAI96076 by the lack of a haemagglutinin tag. A	
CC	XX	claimed method for inhibiting angiogenesis involves transducing an	
CC	XX	epithelial cell with a transgene encoding a CDK1. The transgene	
CC	XX	delivery system is a liposome or a recombinant virus. The CDK1	
CC	XX	is a protein of the CIP/KIP family such as p27, a protein of the	
CC	XX	INK4 family such as p16, active fragments of these (e.g. amino acids	
CC	XX	25-93 or 12-178 of human p27), or a fusion protein comprising 2	
CC	XX	CDK1 proteins such as (truncated) p27 and p16 (see AAI96068-80). A	
CC	XX	method in which the CDK1 is W9 is specifically claimed. The	
CC	XX	method is used to treat conditions associated with angiogenesis,	
CC	XX	e.g. neoplasia, rheumatoid arthritis, endometriosis, psoriasis and	
CC	XX	vascular retinopathy (claimed). Alternatively, the transgene is	

CC delivered to an auxiliary cell, and is expressed by that cell such  
 CC that the CDK1 is released into the blood and contacts the target  
 CC epithelial cell. Use of truncated p27 was designed to increase the  
 CC protein's half-life and to eliminate potential phosphorylation sites  
 CC involved in the negative regulation of CDK1 activity.

XX Sequence 228 AA:

Query Match 81.8%; Score 121; DB 21; Length 228;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPRIOVMNGSARVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLY 87  
 Db 108 alpnapnsygrprigymmgasrvaellllngaepncadpaltlrpvdaaregfltdly 167  
 OY 88 VLHRAGARLDVRDAMGRPLVDLAELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIP 147  
 168 vlhragarldvrdawgrlrvdlaeelghrdvarylraaagtrsgsnharidaegpsdip 227

148 D 148  
 Db 228 d 228

#### RESULT 32

AAW95105  
 ID AAW95105 standard; Protein: 237 AA.

XX AAW95105;

DT 25-MAY-1999 (first entry)

DE Truncated p27/p16 fusion protein.

XX Cyclin-dependent kinase; CDK; cyclin complex; inhibitory; restenosis;  
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acute;  
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
 KW tachycardia; human; p27; p16; truncated.

XX Homo sapiens.

XX MO9906540-A2.

XX 11-FEB-1999.

PF 29-JUL-1998; 98MO-US15759.

PR 29-JUL-1997; 97US-0902572.

XX (MITO-) MITOTIX INC.

PI Beach DH, Gyuris J, Lamphere L;

XX WPI: 1999-153770/13.

DR N-PSDB; AAX26233.

PT Fusion and chimeric proteins including cyclin-dependent kinase  
 PT binding motif - used for regulation of cell proliferation and  
 PT differentiation, for treatment of, e.g. vascular injury, cancers,  
 PT fibrosis and neurodegeneration

PS Claim 63; Page 85; 88pp; English.

XX The invention relates to novel inhibitors of cyclin-dependent kinases  
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
 CC transfection system (A) that comprises: (i) first gene construct  
 CC comprising a sequence encoding an inhibitory polypeptide containing at  
 CC least one CDK-binding motif for binding and inhibiting activity of a

CC CDK, linked to a transcription regulator functional in eukaryotic cells;  
 CC (ii) second gene construct comprising a sequence encoding a polypeptide  
 CC that promotes endothelialisation, and (iii) a gene delivery composition  
 CC for delivering the GCs to a cell for transfection. Also provided are  
 CC nucleic acids encoding a fusion protein (FP) containing: (i) a  
 CC therapeutic polypeptide sequence (TP) from an intracellular protein that  
 CC alters a cellular process when FP enters the cell, and (ii) a  
 CC transcellular polypeptide sequence (TCP) that promotes transcytosis of  
 CC FP. The FP consists of at least one CDK-binding motif and a TCP. See  
 CC AAX26220 for detailed uses of the recombinant transfection system. The  
 CC present sequence represents a human truncated p27/p16 fusion protein.

XX Sequence 237 AA:

Query Match 81.8%; Score 121; DB 20; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPRIOVMNGSARVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLY 87  
 Db 117 alpnapnsygrprigymmgasrvaellllngaepncadpaltlrpvdaaregfltdly 176  
 OY 88 VLHRAGARLDVRDAMGRPLVDLAELGHRDVARYLRAAAGTSGSNHARIDAEGSPDIP 147  
 Db 177 vlhragarldvrdawgrlrvdlaeelghrdvarylraaagtrsgsnharidaegpsdip 236

OY 148 D 148  
 Db 237 d 237

#### RESULT 33

AAW97534  
 ID AAW97534 standard; Protein: 237 AA.

XX AAW97534;

DT 15-JAN-2001 (first entry)

DE Human W9 protein sequence.

XX Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;  
 KW adenovirus E4 protein; neoplasia; W9 protein.

XX Homo sapiens.

XX WO200052184-A1.

PD 08-SEP-2000.

PF 01-MAR-2000; 2000MO-US05350.

PR 01-MAR-1999; 99US-0122974.

PR 08-APR-1999; 99US-0128271.

PR 09-APR-1999; 99US-0128515.

XX (CELL-) CELL GENESYS INC.

PA (MITO-) MITOTIX INC.

DR Patel S, McArthur J, Gyuris J, Mendez MO, Flier M;

XX WPI: 2000-587315/55.

DR N-PSDB; AAA90931.

PS Protein and nucleic acid compositions for preventing and treating

XX neoplasias (particularly cancer), comprises a novel chimeric cyclin

CC dependent kinase inhibitor and adenovirus E4 protein -  
 CC Example 1; Page 119; 126pp; English.  
 CC This sequence represents the human W9 protein.  
 CC The invention relates to a protein composition comprising a novel

CC purified chimeric cyclin dependent kinase inhibitor (CDKi) and a  
 CC purified adenovirus E4 protein. The compositions comprising the protein,  
 CC or the DNA encoding it are useful for treating neoplasias in animals. The  
 CC compositions also find use in assays to eliminate a specific  
 CC sub-population of cultured cells, to determine the susceptibility of  
 CC neoplastic cells to treatment with the compositions and also in assays to  
 CC synchronise cell growth in cultured cells.

XX Sequence 237 AA:

Query Match 81.8%; Score 121; DB 21; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPIQVMMGSAARVAEILLHGAEPCADPATLTRPVHDAAREGFLDTLV 87  
 DB 117 alpnaensygrripqymmgssarvaeilllhgaepncadpatltrpvdaaregfltdltv 176  
 OY 88 VLHRAGARLDVDAWGRLPVDLAELGHRDVARYLRAAAGTGRGSHNARIDAEGPSDIP 147  
 DB 177 vlhregarlvdwdawgrlpvdlaelghrdvarylraaagtrgsnharidaegpsdip 236

OY 148 D 148  
 DB 237 d 237

RESULT 34

AA96049  
 ID AAY96049 standard; Protein; 237 AA.

XX AAY96049;  
 XX  
 DT 05-DEC-2000 (first entry)

DE Antiproliferative truncated p27-p16 fusion protein W9.

XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;  
 KW p16; human; smooth muscle cell; hyperproliferation; restenosis;  
 KM vasotropic; antiproliferative; gene therapy; mutant; mutlein.  
 XX

OS Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Peptide 1..11

FT Protein /label= Haemagglutinin epitope

FT Protein /label= p27(25-93)

FT Protein 94..237

PN WO200052159-A1.

PD 08-SEP-2000.

PF 28-FEB-2000; 2000MO-US04971.

XX 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457568.

PA (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.

PI Mcarthur J, Gyuris J, Finer M;

DR WPI; 2000-594183/56.

DR N-PDB; AAA50496.

XX Novel recombinant lentivirus for inhibiting proliferation of smooth  
 PT muscle cells in e.g. restenosis, is replication deficient and comprises

PT a transgene encoding a cyclin dependent kinase inhibitor -  
 XX  
 PS Example 1; Page 115-116; 126pp; English.

XX The present sequence is that of W9 fusion protein comprising a  
 CC hemagglutinin tag, a truncated human p27 protein (see AAY96048) in  
 CC which only the cyclin dependent kinase inhibitor (CDKi) domain is  
 CC retained, and human p16 protein (see AAY96035). A claimed method for  
 CC inhibiting smooth muscle cell hyperproliferation involves  
 CC transducing smooth muscle cells with a replication-deficient  
 CC recombinant adenovirus that lacks functional E1 and E4 regions, and  
 CC comprises a transgene encoding a CDKi. The CDKi is selected from  
 CC an INK4 family protein such as human p16, a CIP/KIP family protein  
 CC such as p27, active fragments of these, or fusion proteins  
 CC comprising (active fragments of) an INK4 family protein and a  
 CC CIP/KIP family protein (see AAY96046 and AAY96049). A fusion protein  
 CC comprising W9 is specifically claimed. The method is used to  
 CC inhibit mammalian smooth muscle cell hyperproliferation induced  
 CC by injury caused by angioplasty, stent placement or vein  
 CC engraftment. It is useful for treating vascular pathologies e.g.,  
 CC restenosis. Also claimed are recombinant lentiviruses encoding  
 CC CDKis. Use of truncated p27 was designed to increase the protein's  
 CC half-life and to eliminate potential phosphorylation sites involved  
 CC in the negative regulation of CDKi activity. The p27-p16 fusion  
 CC proteins interact with the CDK4/cyclinD, CDK2/cyclinA and  
 CC CDK2/cyclinE complexes and inhibit cell cycle progression at  
 CC multiple points.

XX Sequence 237 AA:

Query Match 81.8%; Score 121; DB 21; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 ALPNAPNSYGRPIQVMMGSAARVAEILLHGAEPCADPATLTRPVHDAAREGFLDTLV 87  
 DB 117 alpnaensygrripqymmgssarvaeilllhgaepncadpatltrpvdaaregfltdltv 176  
 OY 88 VLHRAGARLDVDAWGRLPVDLAELGHRDVARYLRAAAGTGRGSHNARIDAEGPSDIP 147  
 DB 177 vlhregarlvdwdawgrlpvdlaelghrdvarylraaagtrgsnharidaegpsdip 236

OY 148 D 148  
 DB 237 d 237

RESULT 35

AA96076  
 ID AAY96076 standard; Protein; 237 AA.

XX AAY96076;

DT 05-DEC-2000 (first entry)

DE Angiogenesis inhibitor p27(25-93)-p16 fusion W9.

XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; human; p27;  
 KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
 KW endometriosis; psoriasis; vascular retinopathy; cytostatic;  
 KW antiarthritic; antirheumatic; gynaecological; antiapoptotic;  
 KW antiproliferative; gene therapy; mutant; mutlein.

XX Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Peptide 1..11

FT Protein /label= Haemagglutinin epitope

FT Protein 94..237

```

FT      /label= p16
XX
XX      WO200052158-A1.
XX
XX      08-SEP-2000.
XX
XX      28-FEB-2000; 2000WO-US04970.
XX
XX      01-MAR-1999; 99US-0122974.
XX      PR      05-NOV-1999; 99US-0163682.
XX      PR      09-DEC-1999; 99US-0457646.
XX
XX      (CELL-) CELL GENESYS INC.
XX      (MITO-) MITOTIX INC.
XX
XX      Patel S, McArthur J, Gyuris J;
XX
XX      WPI: 2000-565501/52.
XX      DR      N-PSDB; AAA50531.
XX
XX      Inhibiting angiogenesis and treating angiogenesis-associated
XX      conditions, e.g. neoplasia, psoriasis by transducing an endothelial
XX      cell with a recombinant virus having a transgene encoding a cyclin
XX      dependent kinase inhibitor
XX
XX      Example 1; Page 123-124; 138pp; English.
XX
XX      The present sequence is that of fusion protein W9 comprising an
XX      N-terminal haemagglutinin tag, a truncated human p27 protein (see
XX      AAY96075) in which only the cell dependent kinase inhibitory domain
XX      was retained, and a human p16 protein (see AAY96067). A claimed method
XX      for inhibiting angiogenesis involves transducing an epithelial cell
XX      with a transgene encoding a cyclin dependent kinase inhibitor (CDKi).
XX      The delivery system is a liposome or a recombinant virus. The CDKi
XX      is a protein of the Cip/Kip family such as p27, a protein of the
XX      INK4 family such as p16, active fragments of these (e.g. amino acids
XX      25-93 or 12-178 of human p27), or a fusion protein comprising 2
XX      CDKi proteins such as (truncated) p27 and p16 (see AAY96068-80). A
XX      method in which the CDKi is W9 is specifically claimed. The
XX      method is used to treat conditions associated with angiogenesis,
XX      e.g. neoplasia, rheumatoid arthritis, endometriosis, psoriasis and
XX      vascular retinopathy (claimed). Alternatively, the transgene is
XX      delivered to an auxiliary cell, and is expressed by that cell such
XX      that the CDKi is released into the blood and contacts the target
XX      epithelial cell. Use of truncated p27 was designed to increase the
XX      protein's half-life and to eliminate potential phosphorylation sites
XX      involved in the negative regulation of CDKi activity.
XX
XX      Sequence      237 AA:
XX
XX      Query Match      81.8%; Score 121; DB 21; Length 237;
XX      Best Local Similarity 100.0%; Pred. No. 2.3e-108;
XX      Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      28 ALPNAPNSYGRPRIOVMMGSAARVAELLHGAEPNCADPATITLRPVHDAAREGFDTLV 87
XX      |||||||
XX      Db 117 alpnapnsygrprpqvmummgasarvaeellllhgaepncadpatlrrpvhdaaregfldtlv 176
XX
XX      QY 88 VLHRAGARLDVDAWGRILPVDLAEELGHRDVARYLRAAAGTGRGSNNARIDAEGPSDIP 147
XX      |||||||
XX      Db 177 vlhragarldvrdawgrilpvdlaeelghrdrvarylraaagtlgrsnnharidaegpsdip 236
XX
XX      QY 148 D 148
XX      |
XX      Db 237 d 237
XX
XX      RESULT 36
XX      AAW95106
XX      ID AAW95106 standard; Protein; 252 AA.
XX      AC AAW95106;.

```

```

XX      25-MAY-1999 (first entry)
XX
XX      Truncated p27/p16 fusion protein.
XX
XX      Cyclin-dependent kinase; CDK; cyclin complex; inhibitory; restenosis;
XX      CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
XX      intracellular; transcellular; transcytosis; vascular wound; repair; hair;
XX      smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
XX      cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
XX      tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
XX      tachycardia; human; p27; p16; truncated.
XX
XX      Homo sapiens.
XX
XX      WO906540-A2.
XX
XX      11-FEB-1999.
XX
XX      29-JUL-1998; 98WO-US15759.
XX      PF
XX      29-JUL-1997; 97US-0902572.
XX      PR
XX      (MITO-) MITOTIX INC.
XX      PA
XX      Beach DH, Gyuris J, Lamphere L;
XX      PI
XX      WPI: 1999-153770/13.
XX      DR      N-PSDB; AAX26234.
XX
XX      Fusion and chimaeric proteins including cyclin-dependent kinase
XX      binding motif - used for regulation of cell proliferation and
XX      differentiation, for treatment of, e.g. vascular injury, cancers,
XX      fibrosis and neurodegeneration
XX
XX      Claim 63; Page 85; 88pp; English.
XX
XX      The invention relates to novel inhibitors of cyclin-dependent kinases
XX      (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
XX      transfection system (A) that comprises: (i) first gene construct
XX      comprising a sequence encoding an inhibitory polypeptide containing at
XX      least one CDK-binding motif for binding and inhibiting activity of a
XX      CDK, linked to a transcription regulator functional in eukaryotic cells;
XX      (ii) second gene construct comprising a sequence encoding a polypeptide
XX      that promotes endothelialisation, and (iii) a gene delivery composition
XX      for delivering the gcs to a cell for transfection. Also provided are
XX      nucleic acids encoding a fusion protein (FP) containing: (i) a
XX      therapeutic polypeptide sequence (TP) from an intracellular protein that
XX      alters a cellular process when FP enters the cell, and (ii) a
XX      transcellular polypeptide sequence (TCP) that promotes transcytosis of
XX      FP. The FP consists of at least one CDK-binding motif and a TCP. See
XX      AAX26220 for detailed uses of the recombinant transfection system. The
XX      present sequence represents a human truncated p27/p16 fusion protein.
XX
XX      Sequence      252 AA:
XX
XX      Query Match      81.8%; Score 121; DB 20; Length 252;
XX      Best Local Similarity 100.0%; Pred. No. 2.5e-108;
XX      Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      28 ALPNAPNSTYGRPRIOVMMGSAARVAELLHGAEPNCADPATITLRPVHDAAREGFDTLV 87
XX      |||||||
XX      Db 132 alpnapnsygrprpqvmummgasarvaeellllhgaepncadpatlrrpvhdaaregfldtlv 191
XX
XX      QY 88 VLHRAGARLDVDAWGRILPVDLAEELGHRDVARYLRAAAGTGRGSNNARIDAEGPSDIP 147
XX      |||||||
XX      Db 192 vlhragarldvrdawgrilpvdlaeelghrdrvarylraaagtlgrsnnharidaegpsdip 251
XX
XX      QY 148 D 148
XX      |
XX      Db 252 d 252

```

```
RESULT 37
AA97535
ID AAY97535 standard; Protein; 252 AA.
XX
AC AAY97535;
XX
DT 15-JAN-2001 (first entry)
XX
DE Human W10 protein sequence.
XX
KW Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;
adenovirus E4 protein; neoplasia; W10 protein.
XX
OS Homo sapiens.
XX
PN WO200052184-A1.
XX
PD 08-SEP-2000.
XX
PR 01-MAR-2000; 2000WO-US05350.
XX
PR 01-MAR-1999; 99US-0122974.
PR 08-APR-1999; 99US-0128271.
PR 09-APR-1999; 99US-0128515.
XX
PA (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX
PI Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;
DR MPI: 2000-587315/55.
DR N-PSDB; AAA90932.
XX
XX
PT Protein and nucleic acid compositions for preventing and treating
PT neoplasias (particularly cancer), comprises a novel chimeric cyclin
PT dependent kinase inhibitor and adenovirus E4 protein -
XX
PS Example 1; Page 120; 126pp; English.
XX
XX
CC This sequence represents the human W10 protein.
CC The invention relates to a protein composition comprising a novel
CC purified chimeric cyclin dependent kinase inhibitor (CDK1) and a
CC purified adenovirus E4 protein. The compositions comprising the protein,
CC or the DNA encoding it are useful for treating neoplasias in animals. The
CC compositions also find use in assays to eliminate a specific
CC sub-population of cultured cells, to determine the susceptibility of
CC neoplastic cells to treatment with the compositions and also in assays to
CC synchronize cell growth in cultured cells.
XX
SQ Sequence 252 AA;
```

```
Query Match 81.8%; Score 121; DB 21; Length 252;
Best Local Similarity 100.0%; Pred. No. 2.5e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 28 ALPNAPNSYGRPIQYMMGSAKVAELLILGAEPCNDPATLTPVHDAREGFLDITLV 87
|
DB 132 alpnapnsygrripqymmgasrvaellllhgaepncdpatltpvhdaregfltdltv 191
|
QY 88 VLRAGARLDVDWAGRLPYDLAEELGHDVARKYRAAAGGTRGSNHRIDAEGPSDIP 147
|
DB 192 vltregarldvdawgripvdlaeelghdvarkyrraaagtrgsnharidaaegpsdip 251
|
QY 148 D 148
|
DB 252 d 252
```

```
RESULT 38
AA96050
ID AAY96050 standard; Protein; 252 AA.
```

```
XX
AC AAY96050;
XX
DT 05-DEC-2000 (first entry)
XX
DE Antiproliferative truncated p27-p16 fusion protein W10.
XX
KW Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;
p16; human; smooth muscle cell; hyperproliferation; restenosis;
vasotrophic; antiproliferative; gene therapy; mutant; mutein.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..11
FT FT /label= Haemagglutinin_epitope
FT Protein 12..80
FT FT /label= p27(12-178)
FT Peptide 81..95
FT FT /label= Hinge
FT Protein 108..252
FT FT /label= p16
XX
PN WO200052159-A1.
XX
PD 08-SEP-2000.
XX
PR 28-FEB-2000; 2000WO-US04971.
XX
PR 01-MAR-1999; 99US-0122974.
PR 05-NOV-1999; 99US-0163682.
PR 09-DEC-1999; 99US-0457568.
XX
XX
PA (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
XX
XX
PI McArthur J, Gyuris J, Finer M;
DR MPI: 2000-594183/56.
DR N-PSDB; AAA50497.
XX
XX
PT Novel recombinant lentivirus for inhibiting proliferation of smooth
PT muscle cells in e.g. restenosis, is replication deficient and comprises
PT a transgene encoding a cyclin dependent kinase inhibitor -
XX
PS Example 1; Page 116-117; 126pp; English.
XX
XX
CC The present sequence is that of W10 fusion protein comprising a
CC haemagglutinin tag, a truncated human p27 protein (see AAY96048) in
CC which only the cyclin dependent kinase inhibitor (CDK1) domain is
CC retained, a (Gly4Ser)3 hinge, and human p16 protein (see AAY96053). A
CC claimed method for inhibiting smooth muscle cell hyperproliferation
CC involves transducing smooth muscle cells with a replication-deficient
CC recombinant adenovirus that lacks functional E1 and E4 regions, and
CC comprises a transgene encoding a CDK1. The CDK1 is selected from
CC an INK4 family protein such as human p16, a CIP/KIP family protein
CC such as p27, active fragments of these, or fusion proteins
CC comprising (active fragments of) an INK4 family protein and a
CC CIP/KIP family protein (see AAY96046 and AAY96049). The method is used
CC to inhibit mammalian smooth muscle cell hyperproliferation induced
CC by injury caused by angioplasty, stent placement or vein
CC engraftment. It is useful for treating vascular pathologies e.g.,
CC restenosis. Also claimed are recombinant lentiviruses encoding
CC CDK1s. Use of truncated p27 was designed to increase the protein's
CC half-life and to eliminate potential phosphorylation sites involved
CC in the negative regulation of CDK1 activity. The p27-p16 fusion
CC proteins interact with the CDK4/cyclinD, CDK2/cyclinA and
CC CDK2/cyclin complexes and inhibit cell cycle progression at
CC multiple points.
XX
SQ Sequence 252 AA;
```

Query Match 81.8%; Score 121; DB 21; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAFVALLLHGAEPCADPATLTRPVHDAAREGFLDTLV 87  
 |||  
 Db 132 alpnapnsygrpiqymmmgsarvae11llhgaeppcadpatltrpvhdaaregflidtlv 191

QY 88 VLHRAARLDVRDANGRLPYDLAEELGHRDVARYLRAAAGTGRGSHARIDAAREGSPDIP 147  
 |||  
 Db 192 vlhragarldvrdawgrlpydlaeelghrdvarylraaagtrgsharidaaegpsdip 251

QY 148 D 148  
 |  
 Db 252 d 252

RESULT 39  
 AAY96077  
 AAY96077 standard; Protein; 252 AA.

AC AAY96077;  
 DT 05-DEC-2000 (first entry)  
 DE Angiogenesis inhibitor p27(25-93)-p16 fusion W10.  
 XX  
 XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; human; p27;  
 KM angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
 KM endometriosis; psoriasis; vascular retinopathy; cytostatic;  
 KM antiarthritic; antirheumatic; gynaecological; antipsoriatic;  
 KM antiproliferative; gene therapy; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..11  
 FT Protein /label= Haemagglutinin\_epitope  
 FT /label= p27(12-178)  
 FT Peptide 81..95  
 FT /label= Hinge  
 FT 108..252  
 FT Protein /label= p16  
 PN MO200052158-A1.  
 XX  
 XX 08-SEP-2000.  
 PF 28-FEB-2000; 2000WO-US04970.  
 XX  
 PR 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457646.  
 XX  
 PA (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.  
 XX  
 PI Patel S, McArthur J, Gyuris J;  
 XX  
 DR MPI: 2000-565501/52.  
 DR N-PSDB; AAA50532.  
 XX  
 PT Inhibiting angiogenesis and treating angiogenesis-associated  
 PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
 PT cell with a recombinant virus having a transgene encoding a cyclin  
 PT dependent kinase inhibitor -  
 XX  
 PS Example 1; Page 124-125; 138pp; English.  
 XX  
 CC The present sequence is that of fusion protein W10 comprising an

CC N-terminal haemagglutinin tag, a truncated human p27 protein (see  
 CC AAY96075) in which only the cyclin dependent kinase inhibitory domain  
 CC is retained, a (Gly/Ser)<sup>3</sup> hinge, and human p16 protein (see AAY96067).  
 CC A claimed method for inhibiting angiogenesis involves transducing an  
 CC epithelial cell with a transgene encoding a cyclin dependent kinase  
 CC inhibitor (CDK1). The delivery system is a liposome or a recombinant  
 CC virus. The CDK1 is a protein of the CIP/KIP family such as p27, a  
 CC protein of the INK4 family such as p16, active fragments of these  
 CC (e.g. amino acids 25-93 or 12-178 of human p27), or a fusion protein  
 CC comprising 2 CDK1 proteins such as (truncated) p27 and p16 (see  
 CC AAY96068-80). The method is used to treat conditions associated with  
 CC angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis,  
 CC psoriasis and vascular retinopathy (Claimed). Alternatively, the  
 CC transgene is delivered to an auxiliary cell, and is expressed by  
 CC that cell such that the CDK1 is released into the blood and  
 CC contacts the target epithelial cell. Use of truncated p27 was  
 CC designed to increase the protein's half-life and to eliminate  
 CC potential phosphorylation sites involved in the negative  
 CC regulation of CDK1 activity.  
 CC  
 CC Sequence 252 AA;  
 XX  
 XX S0

Query Match 81.8%; Score 121; DB 21; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAFVALLLHGAEPCADPATLTRPVHDAAREGFLDTLV 87  
 |||  
 Db 132 alpnapnsygrpiqymmmgsarvae11llhgaeppcadpatltrpvhdaaregflidtlv 191

QY 88 VLHRAARLDVRDANGRLPYDLAEELGHRDVARYLRAAAGTGRGSHARIDAAREGSPDIP 147  
 |||  
 Db 192 vlhragarldvrdawgrlpydlaeelghrdvarylraaagtrgsharidaaegpsdip 251

QY 148 D 148  
 |  
 Db 252 d 252

RESULT 40  
 AAY96079  
 AAY96079 standard; Protein; 323 AA.

AC AAY96079;  
 DT 05-DEC-2000 (first entry)  
 DE Secretable angiogenesis inhibitor p27(25-93)-p16 fusion W9.  
 XX  
 XX Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; human; p27;  
 KM angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
 KM endometriosis; psoriasis; vascular retinopathy; cytostatic;  
 KM antiarthritic; antirheumatic; gynaecological; antipsoriatic;  
 KM antiproliferative; gene therapy; HIV; protein secretion; mutant;  
 mutein.  
 XX  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Human immunodeficiency virus.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 97..166  
 FT /label= p27(25-93)  
 FT Protein 180..323  
 FT /label= p16  
 PN MO200052158-A1.  
 XX  
 PD 08-SEP-2000.  
 PF 28-FEB-2000; 2000WO-US04970.  
 XX

PR 01-MAR-1999; 99US-0122974.  
PR 05-NOV-1999; 99US-0163682.  
PR 09-DEC-1999; 99US-0457646.  
XX  
PA (CELL-) CELL GENESYS INC.  
XX (MITO-) MITOTIX INC.  
PI Patel S, Mearthur J, Gyuris J;  
XX WPI; 2000-565501/52.  
DR N-PSDB; AAA50534.  
XX  
PT Inhibiting angiogenesis and treating angiogenesis-associated  
PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
PT cell with a recombinant virus having a transgene encoding a cyclin  
PT dependent kinase inhibitor -  
XX  
PS Disclosure: Page 130-131, 138pp; English.

CC The present sequence is that of a secretable, internalizable form  
CC of cyclin dependent kinase inhibitor (CDK1) W9. This version of W9  
CC differs from that of AAY96076 by the inclusion of the proinsulin  
CC leader sequence and a translocation sequence from HIV tat amino  
CC acids 1-72. W9 (see AAY96076) comprises a truncated human p27 protein  
CC (see AAY96075) in which only the cyclin dependent kinase inhibitor  
CC (CDK1) domain is retained, and the human p16 protein (see AAY96067).  
CC A claimed method for inhibiting angiogenesis involves transducing  
CC an epithelial cell with a transgene encoding a CDK1. The CDK1  
CC delivery system is a liposome or a recombinant virus. The CDK1  
CC is a protein of the GIP/KIP family such as p27, a protein of the  
CC INK4 family such as p16, active fragments of these proteins (e.g.  
CC amino acids 25-93 or 12-178 of human p27), or a fusion protein  
CC comprising 2 CDK1 proteins such as (truncated) p27 and p16 (see  
CC AAY96068-80). A method in which the CDK1 is W9 is specifically  
CC claimed. The method is used to treat conditions associated with  
CC angiogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis,  
CC psoriasis and vascular retinopathy (claimed). Alternatively, the  
CC transgene is delivered to an auxiliary cell, and is expressed by  
CC that cell such that the CDK1 is released into the blood and  
CC contacts the target epithelial cell. Use of truncated p27 was  
CC designed to increase the protein's half-life and to eliminate  
CC potential phosphorylation sites involved in the negative  
CC regulation of CDK1 activity.

Sequence 323 AA:

Query Match 81.8%; Score 121; DB 21; Length 323;  
Best Local Similarity 100.0%; Pred. No. 3, 1e-108;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAFYAEILLHGAEPCADPATLTRPVHDAREGFLDTLV 87  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 203 alpnapnsygrripdymmmgasrvaelllllhgaepncadpatltrpvhdaregfltdlv 262  
QY 88 VLRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTSGNSHARIDAAEGSPDIP 147  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 263 vlhragarldvdrwgrlpyvdlaeeighrdvarylraaagtrgsnharidaaegpsdip 322  
QY 148 D 148  
DB |  
DB 323 d 323

RESULT 41

AAW95103 standard; Protein; 334 AA.

AAW95103;

25-MAY-1999 (first entry)

Truncated p27/p16 fusion protein.

XX Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;  
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;  
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;  
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;  
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;  
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;  
KW tachycardia; human; p27; p16; truncated.

OS Homo sapiens.

PN W09906540-A2.

PD 11-FEB-1999.

XX 29-JUL-1998; 98WO-US15759.

XX 29-JUL-1997; 97US-0902572.

XX (MITO-) MITOTIX INC.

XX Beach DH, Gyuris J, Lamphere L;

XX WPI; 1999-153770/13.

XX N-PSDB; AAX26231.

PT Fusion and chimeric proteins including cyclin-dependent kinase  
PT binding motif - used for regulation of cell proliferation and  
PT differentiation, for treatment of, e.g. vascular injury, cancers,  
PT fibrosis and neurodegeneration

PS Claim 63; Page 83; 88pp; English.

CC The invention relates to novel inhibitors of cyclin-dependent kinases  
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
CC transfection system (A) that comprises: (i) first gene construct  
CC comprising a sequence encoding an inhibitory polypeptide containing at  
CC least one CDK-binding motif for binding and inhibiting activity of a  
CC CDK, linked to a transcription regulator functional in eukaryotic cells;  
CC (ii) second gene construct comprising a sequence encoding a polypeptide  
CC that promotes endothelialisation, and (iii) a gene delivery composition  
CC for delivering the GCs to a cell for transfection. Also provided are  
CC nucleic acids encoding a fusion protein (FP) containing: (i) a  
CC therapeutic polypeptide sequence (TP) from an intracellular protein that  
CC alters a cellular process when FP enters the cell, and (ii) a  
CC transcellular polypeptide sequence (TCP) that promotes transcytosis of  
CC FP. The FP consists of at least one CDK-binding motif and a TCP. See  
CC AAX26220 for detailed uses of the recombinant transfection system. The  
CC present sequence represents a human truncated p27/p16 fusion protein.

Sequence 334 AA:

Query Match 81.8%; Score 121; DB 20; Length 334;  
Best Local Similarity 100.0%; Pred. No. 3, 2e-108;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQVMMGSAFYAEILLHGAEPCADPATLTRPVHDAREGFLDTLV 87  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 214 alpnapnsygrripdymmmgasrvaelllllhgaepncadpatltrpvhdaregfltdlv 273  
QY 88 VLRAGARLDVDRAMGRPLPVDLAEEIGHRDVARYLRAAAGTSGNSHARIDAAEGSPDIP 147  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 274 vlhragarldvdrwgrlpyvdlaeeighrdvarylraaagtrgsnharidaaegpsdip 333  
QY 148 D 148  
DB |  
DB 334 d 334

RESULT 42

AAW97532 standard; Protein; 334 AA.

AAW97532

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XX AC AAY97532;
XX DT 15-JAN-2001 (first entry)
XX XX
XX DE Human W8 protein sequence.
XX XX
XX KM Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;
XX KM adenovirus E4 protein; neoplasia; W8 protein.
XX OS Homo sapiens.
XX XX
XX PN WO200052184-A1.
XX PD 08-SEP-2000.
XX PF 01-MAR-2000; 2000WO-US05350.
XX PR 01-MAR-1999; 99US-0122974.
XX PR 08-APR-1999; 99US-0128271.
XX PR 09-APR-1999; 99US-0128515.
XX PA (CELL-) CELL GENESYS INC.
XX PA (MITO-) MITOTIX INC.
XX PI Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;
XX PI WPI: 2000-587315/55.
XX DR N-PSDB: AAA90929.
XX XX
XX PT Protein and nucleic acid compositions for preventing and treating
XX PT neoplasias (particularly cancer), comprises a novel chimeric cyclin
XX PT dependent kinase inhibitor and adenovirus E4 protein -
XX PS Example 1; Page 117-118; 126pp; English.
XX XX
XX CC This sequence represents the human W8 protein.
XX CC The invention relates to a protein composition comprising a novel
XX CC purified chimeric cyclin dependent kinase inhibitor (CDK1) and a
XX CC purified adenovirus E4 protein. The compositions comprising the protein,
XX CC or the DNA encoding it are useful for treating neoplasias in animals. The
XX CC compositions also find use in assays to eliminate a specific
XX CC sub-population of cultured cells, to determine the susceptibility of
XX CC neoplastic cells to treatment with the compositions and also in assays to
XX CC synchronise cell growth in cultured cells.
XX SQ Sequence 334 AA.
XX
XX Query Match 81.8%; Score 121; DB 21; Length 334;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-108;
XX Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX QY 28 ALPNAPNSGSRPIQYMMAGSARVAFELLLHGAEPNCADPATLTTPVHDAAREGLDILY 87
XX |
XX DB 214 alpnapnsygrlpdyymmgasrvaellllhgaepncadpatlttrpvhaareglldtlv 273
XX QY 88 VLRRACARLDVDRAMGRLPVDAEELGHRDVARVYLRRAAGTRGSHARIDAEGPSDIP 147
XX |
XX DB 274 vlrragarldvdarwgrlpvdaeeighrdvarylraaagtrgsharidaaegpsdip 333
XX QY 148 D 148
XX DB 334 d 334

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XX RESULT 43
XX ID AAY96047
XX AC AAY96047 standard; Protein; 334 AA.
XX XX
XX AC AAY96047;
XX XX
XX DT 05-DEC-2000 (first entry)

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```

XX DE Antiproliferative truncated p27-p16 fusion protein W8.
XX KM Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; p27; INK4;
XX KM p16; human; smooth muscle cell; hyperproliferation; restenosis;
XX KM vasotropic; antiproliferative; gene therapy; mutant; mutein.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FT Peptide
XX FT 1..11
XX FT /label= Haemagglutinin_epitope
XX FT 12..176
XX FT /label= p27(12-178)
XX FT Protein
XX FT 177..334
XX FT /label= p16
XX PN WO200052159-A1.
XX PD 08-SEP-2000.
XX PF 28-FEB-2000; 2000WO-US04971.
XX PR 01-MAR-1999; 99US-0122974.
XX PR 05-NOV-1999; 99US-0163682.
XX PR 09-DEC-1999; 99US-0457568.
XX PA (CELL-) CELL GENESYS INC.
XX PA (MITO-) MITOTIX INC.
XX PI McArthur J, Gyuris J, Finer M;
XX DR WPI: 2000-594183/56.
XX DR N-PSDB: AAA50494.
XX XX
XX PT Novel recombinant lentivirus for inhibiting proliferation of smooth
XX PT muscle cells in e.g. restenosis, is replication deficient and comprises
XX PT a transgene encoding a cyclin dependent kinase inhibitor -
XX PS Example 1; Page 113-114; 126pp; English.
XX XX
XX CC The present sequence is that of W8 fusion protein comprising an
XX CC N-terminal haemagglutinin tag, a truncated human p27 protein (see
XX CC AAY96045) in which the first 12 N-terminal and the final 21 C-terminal
XX CC amino acids of full-length p27 (see AAY96052) are deleted, and a
XX CC C-terminal human p16 protein (see AAY96053), with no (Gly/Ser)3 hinge.
XX CC A claimed method for inhibiting smooth muscle cell hyperproliferation
XX CC involves transducing smooth muscle cells with a replication-deficient
XX CC recombinant adenovirus that lacks functional E1 and E4 regions, and
XX CC comprises a transgene encoding a cyclin dependent kinase inhibitor
XX CC (CDK1). The CDK1 is an INK4 family protein such as human p16, a
XX CC CIP/KIP family protein such as p27, active fragments of these, or
XX CC fusion proteins comprising (active fragments of) an INK4 family
XX CC protein and a CIP/KIP family protein (see AAY96046 and AAY96049). The
XX CC method is used to inhibit mammalian smooth muscle cell
XX CC hyperproliferation induced by injury caused by angioplasty, stent
XX CC placement or vein engraftment. It is useful for treating vascular
XX CC pathologies e.g. restenosis. Also claimed are recombinant
XX CC lentiviruses encoding CDK1s. Use of truncated p27 was designed to
XX CC increase the protein's half-life and to eliminate potential
XX CC phosphorylation sites involved in the negative regulation of CDK1
XX CC activity. The p27-p16 fusion proteins interact with the
XX CC CDK4/cyclinD, CDK2/cyclinA and CDK2/cyclinE complexes and inhibit
XX CC cell cycle progression at multiple points.
XX SQ Sequence 334 AA.

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```

XX Query Match 81.8%; Score 121; DB 21; Length 334;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-108;
XX Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 28 ALPNAPNSYGRPIQVMMGSAFVAELLHGAEPNCADPATLTRPVHDAAREGFIDTLV 87  
 DB 214 alpnapnsygrripqymmggsarvaeellllhgaepncadpatltrpvhaaregfidtlv 273  
 QY 88 VLRHAGARLDVDRAMGRPLVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAAGPSDIP 147  
 DB 274 vlrhagarldvdawgrlrvdlaeeighrdvarylraaaggtgrgsnharidaaegpsdip 333  
 QY 148 D 148  
 DB 334 d 334

RESULT 44  
 AAY96074  
 ID AAY96074 standard; Protein: 334 AA.  
 AC AAY96074;  
 XX  
 XX 05-DEC-2000 (first entry)  
 DE Angiogenesis inhibitor p27(12-178)-p16 fusion W8.  
 XX  
 KM Cyclin dependent kinase inhibitor; CDK1; CIP; KIP; human; p27;  
 KM angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
 KM endometriosis; psoriasis; vascular retinopathy; cystostatic;  
 KM antiarthritic; antirheumatic; gynaecological; antipsoriatic;  
 KM antiproliferative; gene therapy; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..11  
 FT /label= Haemagglutinin epitope  
 FT Protein 12..176  
 FT /label= p27(12-178)  
 FT 177..334  
 FT /label= p16  
 PN WO200052158-A1.  
 PD 08-SEP-2000.  
 XX  
 XX 28-FEB-2000; 2000WO-US04970.  
 XX  
 PR 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457646.  
 XX  
 PA (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.  
 XX  
 PI Patel S, Mcarthur J, Gyuris J;  
 DR WPI: 2000-565501/52.  
 DR N-PSDB: AAA50529.  
 XX  
 PT Inhibiting angiogenesis and treating angiogenesis-associated  
 PT conditions, e.g. neoplasia, psoriasis by transducing an endothelial  
 PT cell with a recombinant virus having a transgene encoding a cyclin  
 PT dependent kinase inhibitor -  
 XX  
 XX Example 1; Page 120-122; 138pp; English.  
 CC The present sequence is that of fusion protein W8 comprising an  
 CC N-terminal haemagglutinin tag, a truncated human p27 protein (see  
 CC AAY96072) in which the first 12 N-terminal and the final 21  
 CC C-terminal amino acids of full-length p27 (see AAY96066) are deleted,  
 CC and a C-terminal human p16 protein (see AAY96067). A claimed method  
 CC for inhibiting angiogenesis involves transducing an epithelial cell  
 CC with a transgene encoding a cyclin dependent kinase inhibitor (CDK1).  
 CC The delivery system is a liposome or a recombinant virus. The CDK1

CC is a protein of the CIP/KIP family such as p27, a protein of the  
 CC INK4 family such as p16, active fragments of these (e.g. amino acids  
 CC 25-93 or 12-178 of human p27), or a fusion protein comprising 2 CDK1  
 CC proteins such as (truncated) p27 and p16 (see AAY96068-80). The  
 CC method is used to treat conditions associated with angiogenesis,  
 CC e.g. neoplasia, rheumatoid arthritis, endometriosis, psoriasis and  
 CC vascular retinopathy (claimed). Alternatively, the transgene is  
 CC delivered to an auxiliary cell, and is expressed by that cell such  
 CC that the CDK1 is released into the blood and contacts the target  
 CC epithelial cell. Use of truncated p27 was designed to increase the  
 CC protein's half-life and to eliminate potential phosphorylation sites  
 CC involved in the negative regulation of CDK1 activity.  
 XX  
 SQ Sequence 334 AA;  
 QY 28 ALPNAPNSYGRPIQVMMGSAFVAELLHGAEPNCADPATLTRPVHDAAREGFIDTLV 87  
 DB 214 alpnapnsygrripqymmggsarvaeellllhgaepncadpatltrpvhaaregfidtlv 273  
 QY 88 VLRHAGARLDVDRAMGRPLVDLAEEIGHRDVARYLRAAAGGTRGSNHARIDAAGPSDIP 147  
 DB 274 vlrhagarldvdawgrlrvdlaeeighrdvarylraaaggtgrgsnharidaaegpsdip 333  
 QY 148 D 148  
 DB 334 d 334

RESULT 45  
 AAM23536  
 ID AAM23536 standard; Protein: 365 AA.  
 AC AAM23536;  
 XX  
 XX 16-MAR-1998 (first entry)  
 DE CDK inhibitory fusion protein p16p27.  
 XX  
 XX  
 KM Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;  
 KM chimeric polypeptide; human; binding motif; proliferation control;  
 KM cell differentiation; cell-cycle inhibitor; proliferative disorder;  
 KM tissue degeneration; therapy.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO9727297-A1.  
 PD 31-JUL-1997.  
 XX  
 PF 17-JAN-1997; 97WO-US00569.  
 XX  
 PR 23-JAN-1996; 96US-0589981.  
 XX  
 PA (MITO-) MITOTIX INC.  
 PI Beach D, Gyuris J, Lamphere L;  
 DR WPI: 1997-393685/36.  
 DR N-PSDB: AAT74053.  
 XX  
 PT Chimeric inhibitor of cyclin dependent kinase - useful for gene  
 PT therapy of cancer and other proliferative and differentiative  
 PT diseases  
 XX  
 XX Claim 40; Page 46-48; 58pp; English.  
 CC This sequence represents a chimeric polypeptide of the invention. It was  
 CC derived from a fusion of the human p27 and p16 cDNA sequences. The

CC chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)  
 CC binding motifs from at least two different proteins that bind to CDKs.  
 CC The protein controls proliferation and/or differentiation of cells,  
 CC particularly they inhibit cell-cycle progression. They can be used to  
 CC treat a wide range of proliferative disorders, e.g. cancer, leukemia,  
 CC psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They  
 CC can also treat diseases associated with de-differentiation or  
 CC degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's  
 CC diseases, gastric ulcers and autonomous diseases of the peripheral  
 CC nervous system. Other applications include reducing growth of hair and  
 CC protecting hair follicle cells against cytotoxic treatments, cosmetically  
 CC to treat various forms of folliculitis, and to inhibit spermatogenesis or  
 CC oogenesis. The chimeric proteins can also be used in vitro to maintain  
 CC cells, especially neurons intended for testing specific activity of  
 CC trophic factors, at selected points in the cell cycle. The proteins are  
 CC more active inhibitors of the CDK/cyclin complex than binding motifs used  
 CC individually (since they may bind to CDK involved in different stages of  
 CC the cell cycle).

XX Sequence 365 AA;

Query Match 81.8%; Score 121; DB 16; Length 365;

Best Local Similarity 100.0%; Pred. No. 3.5e-108; Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRRPVQVMWMSARVAELLHGAEPNCADPATLTPVYHDAAREGFLDTLV 87

Db 46 alpnapnsygrripqymmmgsarvae111hgaepncadpatltpvhdaregflidtlv 105

QY 88 VLHRAGARLDVBDAMGRLPVDLAELGHRDVARYLRAAAGTSGSNHARIDAAEGSPDIP 147

Db 106 vlhragarldvbdawgrlpvdlaeelghrdvarylraaagtgsgsnharidaaegspdlp 165

QY 148 D 148

Db 166 d 166

RESULT 46

AAW95107

ID AAW95107 standard; Protein; 365 AA.

AC AAW95107;

DT 25-MAY-1999 (first entry)

XX Human p16p27 fusion protein.

DE Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;

KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;

KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;

KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;

KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;

KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;

KW tachycardia; human; p27; p16.

XX Homo sapiens.

OS MO9906540-A2.

PN 11-FEB-1999.

PD 29-JUL-1998; 98WO-US15759.

XX 29-JUL-1997; 97US-0902572.

PA (MITO-) MITOTIX INC.

XX Fusion and chimeric proteins including cyclin-dependent kinase  
 PT binding motif - used for regulation of cell proliferation and  
 PT differentiation, for treatment of, e.g. vascular injury, cancers,  
 PT fibrosis and neurodegeneration  
 XX Claim 63; Page 86; 88pp; English.

XX The invention relates to novel inhibitors of cyclin-dependent kinases

CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant

CC transfection system (A) that comprises: (i) first gene construct

CC comprising a sequence encoding an inhibitory polypeptide containing at

CC least one CDK-binding motif for binding and inhibiting activity of a

CC CDK, linked to a transcription regulator functional in eukaryotic cells;

CC (ii) second gene construct comprising a sequence encoding a polypeptide

CC that promotes endothelialisation, and (iii) a gene delivery composition

CC for delivering the GCS to a cell for transfection. Also provided are

CC nucleic acids encoding a fusion protein (FP) containing: (i) a

CC therapeutic polypeptide sequence (TP) from an intracellular protein that

CC alters a cellular process when FP enters the cell, and (ii) a

CC transcellular polypeptide sequence (TCP) that promotes transcytosis of

CC CC FP. The FP consists of at least one CDK-binding motif and a TCP. See

CC AAX6220 for detailed uses of the recombinant transfection system. The

CC present sequence represents a human p16p27 fusion protein.

XX Sequence 365 AA;

Query Match 81.8%; Score 121; DB 20; Length 365;

Best Local Similarity 100.0%; Pred. No. 3.5e-108; Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRRPVQVMWMSARVAELLHGAEPNCADPATLTPVYHDAAREGFLDTLV 87

Db 245 alpnapnsygrripqymmmgsarvae111hgaepncadpatltpvhdaregflidtlv 304

QY 88 VLHRAGARLDVBDAMGRLPVDLAELGHRDVARYLRAAAGTSGSNHARIDAAEGSPDIP 147

Db 305 vlhragarldvbdawgrlpvdlaeelghrdvarylraaagtgsgsnharidaaegspdlp 364

QY 148 D 148

Db 365 d 365

RESULT 47

AAW95096

ID AAW95096 standard; Protein; 365 AA.

AC AAW95096;

DT 25-MAY-1999 (first entry)

XX Human p16p27 fusion protein.

DE Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;

KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;

KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;

KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;

KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;

KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;

KW tachycardia; human; p27; p16.

XX Homo sapiens.

OS MO9906540-A2.

PN 11-FEB-1999.

PD 29-JUL-1998; 98WO-US15759.

XX 29-JUL-1997; 97US-0902572.

PA (MITO-) MITOTIX INC.

XX Beach, DR, Gyuris J, Lamphere L;

XX WPI; 1999-153770/13.

XX N-PSDB; AAX6235.

XX

PA (MITO-) MITOTIX INC.  
 XX Beach DH, Gyuris J, Lamphere L;  
 PI WPI; 1999-153770/13.  
 DR N-PSDB; AAX26224.  
 XX  
 PT Fusion and chimeric proteins including cyclin-dependent kinase  
 PT binding motif - used for regulation of cell proliferation and  
 PT differentiation, for treatment of, e.g. vascular injury, cancers,  
 PT fibrosis and neurodegeneration  
 XX  
 PS Claim 63; Page 78-79; 88pp; English.  
 XX  
 CC The invention relates to novel inhibitors of cyclin-dependent kinases  
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant  
 CC transfection system (A) that comprises: (i) first gene construct  
 CC comprising a sequence encoding an inhibitory polypeptide containing at  
 CC least one CDK-binding motif for binding and inhibiting activity of a  
 CC CDK, linked to a transcription regulator functional in eukaryotic cells;  
 CC (ii) second gene construct comprising a sequence encoding a polypeptide  
 CC that promotes endothelialisation, and (iii) a gene delivery composition  
 CC for delivering the GCs to a cell for transfection. Also provided are  
 CC nucleic acids encoding a fusion protein (FP) containing: (i) a  
 CC therapeutic polypeptide sequence (TP) from an intracellular protein that  
 CC alters a cellular process when FP enters the cell, and (ii) a  
 CC transcellular polypeptide sequence (TCP) that promotes transcytosis of  
 CC FP. The FP consists of at least one CDK-binding motif and a TCP. See  
 CC AAX26220 for detailed uses of the recombinant transfection system. The  
 CC present sequence represents a human p16p27 fusion protein.  
 XX  
 SO Sequence 365 AA;  
 50

Query Match 81.8%; Score 121; DB 20; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQYMMGSAFVAELLLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
 Db 46 alpnapnsygrripqymmmgsarvae11llhgaepncadpatltrpvhdaregfldtlv 105  
 QY 88 VLRHAGARLDVPRAMGRPLVDLAEELGHRDVARYLRAAAGTRGSNHARIDAAGPSDIP 147  
 Db 106 vlhagarlidvrdawgrlpvdlaeelghrdvarylraaagtrgsnharidaagpsdip 165  
 QY 148 D 148  
 Db 166 d 166

RESULT 48  
 AAY97527  
 ID AAY97527 standard; Protein: 365 AA.  
 XX  
 AC AAY97527;  
 XX  
 DT 15-JAN-2001 (first entry)  
 XX  
 DE Human W4 protein sequence.  
 XX  
 KW Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;  
 KW adenovirus E4 protein; neoplasia; W4 protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200052184-A1.  
 XX  
 PD 08-SEP-2000.  
 XX  
 PF 01-MAR-2000; 2000WO-US05350.  
 XX  
 PR 01-MAR-1999; 99US-0122974.  
 PR

PR 08-APR-1999; 99US-0128271.  
 PR 09-APR-1999; 99US-0128515.  
 XX  
 PA (MITO-) MITOTIX INC.  
 PI Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;  
 XX  
 XX WPI; 2000-587315/55.  
 DR N-PSDB; AAA90924.  
 XX  
 PT protein and nucleic acid compositions for preventing and treating  
 PT neoplasias (particularly cancer), comprises a novel chimeric cyclin  
 PT dependent kinase inhibitor and adenovirus E4 protein -  
 XX  
 PS Example 1; Page 110-111; 126pp; English.  
 XX  
 CC This sequence represents the human W4 protein.  
 CC The invention relates to a protein composition comprising a novel  
 CC purified chimeric cyclin dependent kinase inhibitor (CDK1) and a  
 CC or the DNA encoding it are useful for treating neoplasias in animals. The  
 CC compositions also find use in assays to eliminate a specific  
 CC sub-population of cultured cells, to determine the susceptibility of  
 CC neoplastic cells to treatment with the compositions and also in assays to  
 CC synchronise cell growth in cultured cells.  
 XX  
 SO Sequence 365 AA;  
 50

Query Match 81.8%; Score 121; DB 21; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPIQYMMGSAFVAELLLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
 Db 245 alpnapnsygrripqymmmgsarvae11llhgaepncadpatltrpvhdaregfldtlv 304  
 QY 88 VLRHAGARLDVPRAMGRPLVDLAEELGHRDVARYLRAAAGTRGSNHARIDAAGPSDIP 147  
 Db 305 vlhagarlidvrdawgrlpvdlaeelghrdvarylraaagtrgsnharidaagpsdip 364  
 QY 148 D 148  
 Db 365 d 365

RESULT 49  
 AAY97529  
 ID AAY97529 standard; Protein: 365 AA.  
 XX  
 AC AAY97529;  
 XX  
 DT 15-JAN-2001 (first entry)  
 XX  
 DE Human W6 protein sequence.  
 XX  
 KW Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;  
 KW adenovirus E4 protein; neoplasia; W6 protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200052184-A1.  
 XX  
 PD 08-SEP-2000.  
 XX  
 PF 01-MAR-2000; 2000WO-US05350.  
 XX  
 PR 01-MAR-1999; 99US-0122974.  
 PR 08-APR-1999; 99US-0128271.  
 PR 09-APR-1999; 99US-0128515.  
 XX  
 PA (CELL-) CELL GENESYS INC.

PA (MITO-) MITOTIX INC.  
 XX  
 XX Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;  
 XX WPI, 2000-587315/55.  
 DR N-PSDB: AAA90926.  
 XX  
 XX Protein and nucleic acid compositions for preventing and treating  
 PT neoplasias (particularly cancer), comprises a novel chimeric cyclin  
 PT dependent kinase inhibitor and adenovirus E4 protein -  
 XX  
 XX Example 1: Page 113-114; 126pp: English.  
 PS  
 XX This sequence represents the human W6 protein.  
 CC The invention relates to a protein composition comprising a novel  
 CC purified chimeric cyclin dependent kinase inhibitor (CDKI) and a  
 CC purified adenovirus E4 protein. The compositions comprising the protein,  
 CC or the DNA encoding it are useful for treating neoplasias in animals. The  
 CC compositions also find use in assays to eliminate a specific  
 CC sub-population of cultured cells, to determine the susceptibility of  
 CC neoplastic cells to treatment with the compositions and also in assays to  
 CC synchronise cell growth in cultured cells.  
 XX  
 XX Sequence 365 AA:  
 SQ  
 XX  
 XX Query Match 81.8%; Score 121; DB 21; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 28 ALPNAPNSYGRRIQVMNMGSAFVAELLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
 DB 46 alpnapnsygrripqymmgasrvaellllhgaepncadpatltrpvhdaregfltdtlv 105  
 OY 88 VLRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTGRGSHARIDAEGPSDIP 147  
 DB 106 vlhragarldvrdawgrlpydlaeelghrdvarylraaagtrgsharidaegpsdip 165  
 OY 148 D 148  
 DB 166 d 166  
 RESULT 50  
 AAY96042  
 ID AAY96042 standard; Protein; 365 AA.  
 XX  
 AC AAY96042;  
 XX  
 XX 05-DEC-2000 (first entry)  
 DE Antiproliferative p27-p16 fusion protein W4.  
 XX  
 XX Cyclin dependent kinase inhibitor; CDKI; CIP; KIP; p27; INK4;  
 KM p16; human; smooth muscle cell; hyperproliferation; restenosis;  
 KM vasotrophic; antiproliferative; gene therapy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..11  
 FT /label= Haemagglutinin\_tag  
 FT Protein 12..208  
 FT /label= p27  
 FT Protein 212..365  
 FT /label= p16  
 FT Misc-difference 15  
 FT /note= "encoded by CGA"  
 FT Misc-difference 149  
 FT /note= "encoded by GAG"  
 XX  
 XX W0200052199-A1.

XX  
 PD 08-SEP-2000.  
 XX  
 XX 28-FEB-2000; 2000MO-US04971.  
 PF  
 XX  
 PR 01-MAR-1999; 99US-0122974.  
 PR 05-NOV-1999; 99US-0163682.  
 PR 09-DEC-1999; 99US-0457568.  
 XX  
 XX (CELL-) CELL GENESYS INC.  
 PA (MITO-) MITOTIX INC.  
 XX  
 XX McArthur J, Gyuris J, Finer M;  
 PI WPI, 2000-594183/56.  
 DR N-PSDB: AAA50489.  
 DR  
 XX  
 XX Novel recombinant lentivirus for inhibiting proliferation of smooth  
 PT muscle cells in e.g. restenosis, is replication deficient and comprises  
 PT a transgene encoding a cyclin dependent kinase inhibitor -  
 XX  
 XX Example 1: Page 103-105; 126pp: English.  
 PS  
 XX  
 XX The present sequence is that of p27-p16 fusion protein W4 comprising  
 CC an N-terminal haemagglutinin tag, the human p27 protein (see AAY96052),  
 CC and the human p16 protein (see AAY96053), with no (Gly4Ser)3 hinge.  
 CC It is encoded by a nucleic acid obtained by PCR amplification of p27  
 CC and p16 DNAs. A claimed method for inhibiting smooth muscle cell  
 CC hyperproliferation involves transducing smooth muscle cells with a  
 CC replication-deficient recombinant adenovirus that lacks functional  
 CC E1 and E4 regions, and comprises a transgene encoding a cyclin  
 CC dependent kinase inhibitor (CDKI). The CDKI is selected from an  
 CC INK4 family protein such as human p16, a CIP/KIP family protein  
 CC such as p27, active fragments of these, or fusion proteins  
 CC comprising (active fragments of) an INK4 family protein and a  
 CC CIP/KIP family protein (see AAY96046 and AAY96049). The method is used  
 CC to inhibit mammalian smooth muscle cell hyperproliferation, induced  
 CC by injury caused by angioplasty, stent placement or vein  
 CC engraftment. It is useful for treating vascular pathologies e.g.,  
 CC restenosis. Also claimed are recombinant lentiviruses encoding  
 CC CDKIs.  
 XX  
 XX Sequence 365 AA:  
 SQ  
 XX  
 XX Query Match 81.8%; Score 121; DB 21; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-108;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 28 ALPNAPNSYGRRIQVMNMGSAFVAELLHGAEPNCADPATLTRPVHDAREGFLDTLV 87  
 DB 245 alpnapnsygrripqymmgasrvaellllhgaepncadpatltrpvhdaregfltdtlv 304  
 OY 88 VLRAGARLDVDAWGRLPYDLAEELGHRDVARYLRAAAGTGRGSHARIDAEGPSDIP 147  
 DB 305 vlhragarldvrdawgrlpydlaeelghrdvarylraaagtrgsharidaegpsdip 364  
 OY 148 D 148  
 DB 365 d 365  
 Search completed: September 19, 2002, 17:28:32  
 Job time: 245 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 19, 2002, 17:27:07 ; Search time 16.1 Seconds

(without alignments)  
883.306 Million cell updates/sec

Title: us-09-016-869b-35

Perfect score: 148  
Sequence: 1 MEPSADWLTATAARGVEEV.....TRGSNHARIDAAEGSPDIPD 148

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

W size: 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database : PIR\_71:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	121	81.8	156	2	JE0141	cyclin dependent k
2	72	48.6	138	2	B53479	CDK4 inhibitor p14
3	48	32.4	130	2	I78845	p15INK4b - mouse
4	34	23.0	41	2	I52720	gene p15INK4b prot
5	19	12.8	167	2	I68352	p16INK4a - mouse
6	8	5.4	334	2	G69303	iron (III) ABC tra
7	8	5.4	390	2	T43647	hypothetical prote
8	5.4	1691	1	A44212	genome polyprotein	
9	5.4	1693	1	MMWME	genome polyprotein	
10	4.7	138	2	AD1515	hypothetical prote	
11	4.7	138	2	AD1156	hypothetical prote	
12	4.7	141	2	AB1892	hypothetical prote	
13	4.7	142	2	B72683	hypothetical prote	
14	4.7	154	1	A70792	hypothetical prote	
15	4.7	160	2	E34768	ORF3 protein - Orf	
16	4.7	164	2	A57378	cyclin-dependent k	
17	4.7	166	2	A57379	CDK4/CDK6 inhibito	
18	4.7	166	2	B57378	cyclin-dependent k	
19	4.7	171	2	E97641	hypothetical prote	
20	4.7	171	2	AF2864	acetyltransferase	
21	4.7	173	2	AI1885	hypothetical prote	
22	4.7	195	2	T36141	hypothetical prote	
23	4.7	205	2	C88814	probable nicotinam	
24	4.7	216	2	AH3203	Rhtb family transp	
25	4.7	223	1	B23724	alcohol dehydrogen	
26	4.7	223	1	C23724	alcohol dehydrogen	
27	4.7	223	1	D23724	alcohol dehydrogen	
28	4.7	227	2	A75304	ABC transporter, A	
29	4.7	229	2	H83425	probable enoyl-CoA	

30	7	4.7	230	2	A95886	probable transcrip
31	7	4.7	231	2	D69880	purine nucleoside
32	7	4.7	251	2	F82977	transcription regu
33	7	4.7	254	1	DEFERL	alcohol dehydrogen
34	7	4.7	254	1	A40553	alcohol dehydrogen
35	7	4.7	254	1	S15711	alcohol dehydrogen
36	7	4.7	254	1	S15712	alcohol dehydrogen
37	7	4.7	254	1	S06001	alcohol dehydrogen
38	7	4.7	254	1	B24268	alcohol dehydrogen
39	7	4.7	254	1	A24268	alcohol dehydrogen
40	7	4.7	254	1	S01901	alcohol dehydrogen
41	7	4.7	254	1	E23724	alcohol dehydrogen
42	7	4.7	254	2	A23724	alcohol dehydrogen
43	7	4.7	254	2	D72464	hypothetical prote
44	7	4.7	273	2	T34740	hypothetical prote
45	7	4.7	278	2	F87289	molybdenum transpo
46	7	4.7	283	2	E84258	hypothetical prote
47	7	4.7	314	2	D70313	riboflavin kinase
48	7	4.7	318	1	F70536	3',5'-cyclic-nucle
49	7	4.7	331	2	D86413	cysteine proteinas
50	7	4.7	333	2	JC7713	ankyrin-repeat pro
51	7	4.7	334	2	A82751	ABC transporter AT
52	7	4.7	345	2	B84752	probable cysteine
53	7	4.7	346	2	C86413	cysteine proteinas
54	7	4.7	348	2	T18230	alcohol dehydrogen
55	7	4.7	348	2	T35450	ABC transporter AT
56	7	4.7	353	2	D75553	branched-chain aml
57	7	4.7	363	2	E75457	probable phosphata
58	7	4.7	364	2	C70777	probable cobC - My
59	7	4.7	365	2	F86413	probable cysteine
60	7	4.7	389	2	E82618	hypothetical prote
61	7	4.7	405	2	F86314	protein F2H15.16 l
62	7	4.7	413	2	D70668	probable transposa
63	7	4.7	462	2	B75306	probable cyclopro
64	7	4.7	464	2	AE2650	glutamine syntheta
65	7	4.7	466	1	MMBHT	capsid protein ICP
66	7	4.7	479	2	D97432	probable glutamine
67	7	4.7	504	2	B98159	argininosuccinate
68	7	4.7	504	2	AG3128	argininosuccinate
69	7	4.7	507	2	C97499	guanosine-5'-triph
70	7	4.7	507	2	AH2717	exopolysphatase
71	7	4.7	512	2	AF3402	hypothetical prote
72	7	4.7	520	2	C70311	hypothetical prote
73	7	4.7	523	2	C70717	probable purif prot
74	7	4.7	527	1	ORSEUB	stib protein - Ser
75	7	4.7	527	2	T37055	probable oxidoredu

#### ALIGNMENTS

RESULT 1  
JE0141  
N:Alternate names: CDK4 inhibitor p16 (INK4A/MIS1); cyclin-dependent kinase inhibitor  
C:Species: Homo sapiens (man)  
C>Date: 02-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 19-May-2000  
C:Accession: JE0141; 159268; S39359; 159585; JC5679  
R:Huang, C.G.; Deng, W.; Fu, J.L.  
Chin, J. Biotechnol. 13, 105-107, 1997  
A:Title: Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.  
A:Reference number: JE0141  
A:Accession: JE0141  
A:Molecule type: mRNA  
A:Residues: 1-156 <HUA>  
A:Experimental source: Hella cell  
R:Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett,  
Proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994  
A:Title: Mutations and altered expression of p16INK4 in human cancer.  
A:Reference number: 159268; WUID:95062202  
A:Accession: 159268  
A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A:Residues: 1-152 <KAM>  
A:Cross-references: GB:L27211; NID:9558656; PIDN:AAA92554.1; PID:9558657  
A:Note: The sequence is revised in Genbank entry HUMINK4X, release 113.0, PIDN:AAA92554.1  
R:Serano, M.; Hannon, G.J.; Beach, D.  
Nature 356, 704-707, 1993  
A:Title: A new regulatory motif in cell-cycle control causing specific inhibition of cyclin D  
A:Reference number: S39359; MUID:94081956  
A:Accession: S39359  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 9-34, 'V', 36-156 <SER>  
A:Note: this sequence is corrected in reference I59268  
R:Hann, A.; Gruts, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Science 264, 436-440, 1994  
A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.  
A:Reference number: I59585; MUID:94204645  
A:Accession: I59585  
A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 51-152 <KAM>  
A:Cross-references: GB:S69804; NID:9546272; PIDN:AAD14048.1; PID:94261748  
A:Note: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 kinase  
C:Genetics:  
A:Gene: GDB:CDKN2A; CDK4I; MIM: P16; INK4; MTS1; CMM2; CDKN2  
A:Cross-references: GDB:335362; OMIM:600160  
A:Map position: 9p21-9p21  
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology  
C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match  
Best Local Similarity 100.0%; Score 121; DB 2; Length 156;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ALPNAPNSYGRPRIOYMMGSAVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87  
Db 36 ALPNAPNSYGRPRIOYMMGSAVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95

QY 88 VLRAGARLDVDRAGRLPVDAELGHRDVARVLRPAAGTGRSGNHARIDAEGSDIP 147  
Db 96 VLRAGARLDVDRAGRLPVDAELGHRDVARVLRPAAGTGRSGNHARIDAEGSDIP 155

QY 148 D 148  
Db 156 D 156

RESULT 2  
79 Inhibitor p14(INK4B/MTS2) - human  
N:Alternate names: CDK6-associated protein p15(INK4B); cyclin-dependent kinase inhibitor  
C:Species: Homo sapiens (man)  
C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 21-Jul-2000  
C:Accession: B55479; S47593; I81183; I52713  
R:Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.; Genes Dev. 8, 2939-2952, 1994  
A:Title: Growth suppression by p18, a p16(INK4/MTS1) - and p14(INK4B/MTS2)-related CDK6 A  
A:Reference number: A55479; MUID:95095079  
A:Accession: B55479  
A:Molecule type: mRNA  
A:Residues: 1-138 <GUA>  
A:Cross-references: GB:U17075; NID:9639715; PIDN:AAC50075.1; PID:9639716  
A:Experimental source: HeLa cells  
R:Hannon, G.J.; Beach, D.  
Nature 371, 257-261, 1994  
A:Title: p15(INK4B) is a potential effector of TGF-beta-induced cell cycle arrest.  
A:Reference number: S47593; MUID:94359613  
A:Accession: S47593  
A:Molecule type: mRNA  
A:Residues: 1-19, 'TP', 22-24-31, 'HSW', 35-138 <HAN>  
A:Cross-references: GB:I36844; NID:9556197; PIDN:AAA50282.1; PID:9556198  
A:Experimental source: HaCat cells  
R:Kamb, P.; Grits, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; St

Science 264, 436-440, 1994  
A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.  
A:Reference number: I59585; MUID:94204645  
A:Accession: I81183  
A:Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 53-138 <KAM>  
A:Cross-references: GB:S69805; NID:9546273; PIDN:AAD14049.1; PID:94261749  
R:Jen, J.; Harper, J.W.; Bigner, S.H.; Bigner, D.D.; Papadopoulos, N.; Markowitz, S.; Cancer Res. 54, 6353-6358, 1994  
A:Title: Deletion of p16 and p15 genes in brain tumors.  
A:Reference number: I52713; MUID:95079408  
A:Accession: I52713  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-52 <RES>  
A:Cross-references: GB:S75756; NID:9861470; PIDN:AAD14186.1; PID:94261886  
C:Genetics:  
A:Gene: GDB:CDKN2B; MTS2  
A:Cross-references: GDB:579577; OMIM:600431  
A:Map position: 9p21-9p21  
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology  
C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match  
Best Local Similarity 100.0%; Score 72; DB 2; Length 138;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IOVMMGSAVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLVLRAGARLDVDR 100  
Db 51 IOVMMGSAVAELLHGAEPNCADPATLTRPVHDAAREGFLDTLVLRAGARLDVDR 110

QY 101 AMGRLPVDAEE 112  
Db 111 AMGRLPVDAEE 122

RESULT 3  
178845 p15INK4b - mouse  
C:Species: Mus sp. (mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 19-May-2000  
C:Accession: I78845  
R:Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H. Oncogene 11, 635-645, 1995  
A:Title: Cloning and characterization of murine p16INK4a and p15INK4b genes.  
A:Reference number: I58352; MUID:95380169  
A:Accession: I78845  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-130 <RES>  
A:Cross-references: GB:S79252; NID:91087092; PID:91087093  
C:Genetics:  
A:Gene: p15INK4b  
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

Query Match  
Best Local Similarity 100.0%; Score 48; DB 2; Length 130;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VAEILLHGAEPNCADPATLTRPVHDAAREGFLDTLVLRAGARLDV 98  
Db 53 VAEILLHGAEPNCADPATLTRPVHDAAREGFLDTLVLRAGARLDV 100

RESULT 4  
152720 p15INK4b protein - rat (fragment)  
C:Species: Rattus sp. (rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 26-May-2000  
C:Accession: I52720

R:Knapik, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.

Cancer Res. 55, 1607-1612, 1995

A:Title: Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in kidney epithelial

A:Reference number: 152720; MUID:95228036

A:Accession: 152720

A>Status: preliminary; translated from GB/EMBL/DDJ

A:Molecule type: DNA

A:Residues: 1-41 <RES>

A:Cross-references: GB:S77734; NID:9998711

C:Genetics:

C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

Query Match 23.0%; Score 34; DB 2; Length 41;

Best Local Similarity 100.0%; Pred. No. 2.8e-26;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 VAEILLHGAEPNCADPATLTRPVHDAAREGFD 84

8 VAEILLHGAEPNCADPATLTRPVHDAAREGFD 41

RESULT 5

I58352

p16INK4a - mouse

C:Species: Mus sp. (mouse)

C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 24-Nov-1999

C:Accession: I58352

R:Quelle, D.E.; Ashmun, R.A.; Hannou, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.; W

Oncogene 11, 635-645, 1995

A:Title: Cloning and characterization of murine p16INK4a and p15INK4b genes.

A:Reference number: I58352; MUID:95380169

A:Accession: I58352

A>Status: preliminary; translated from GB/EMBL/DDJ

A:Molecule type: mRNA

A:Residues: 1-167 <RES>

A:Cross-references: GB:S79251; NID:91087090; PID:91087091

C:Genetics:

C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

Query Match 12.8%; Score 19; DB 2; Length 167;

Best Local Similarity 100.0%; Pred. No. 5.7e-11;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 RPVHDAAREGFDLTVLH 90

1 71 RPVHDAAREGFDLTVLH 89

RESULT 6

G69303

Iron (III) ABC transporter, permease protein (hemu-1) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Aug-1999

C:Accession: G69303

R:Rieck, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Nature 390, 364-370, 1997

A:Authors: Utechtack, T.; Cotton, M.D.; Spriggs, T.; Airlach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Moese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A:Accession: G69303

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-334 <RES>

A:Cross-references: GB:AE001075; GB:AE000782; NID:92689398; PIDN:AAB90806.1; PID:9265020

Query Match 5.4%; Score 8; DB 2; Length 334;

Best Local Similarity 100.0%; Pred. No. 7.1;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 RVAEILL 57

9 RVAEILL 16

RESULT 7

T43647

hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)

C:Species: Schizosaccharomyces pombe

C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000

C:Accession: T43647

R:Lee, M.; Yoo, H.S.; Chung, K.S.

submitted to the EMBL Data Library, February 1998

A:Description: Clone 17 (blind homologue).

A:Reference number: 222596

A:Accession: T43647

A>Status: preliminary; translated from GB/EMBL/DDJ

A:Molecule type: mRNA

A:Residues: 1-390 <LEE>

A:Cross-references: EMBL:AF049529; PIDN:AAD02493.1

Query Match 5.4%; Score 8; DB 2; Length 390;

Best Local Similarity 100.0%; Pred. No. 8.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 122 LRAAAGT 129

15 LRAAAGT 22

RESULT 8

A44212

genome polypeptide - hepatitis E virus (strain Mexico)

N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)

C:Species: hepatitis E virus

C>Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 19-Jan-2001

C:Accession: A44212; B48547

R:Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A

Virology 191, 550-558, 1992

A:Title: Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus

A:Reference number: A44212; MUID:93079857

A:Accession: A44212

A:Molecule type: genomic RNA

A:Residues: 1-1691 <HUA>

A:Cross-references: GB:M74506; NID:9330017; PIDN:AAA45730.1; PID:9330018

R:Fry, K.E.; Tam, A.W.; Smith, M.M.; Kim, J.P.; Luk, K.C.; Young, L.M.; Platak, M.; F

Virus Genes 6, 173-185, 1992

A:Title: Hepatitis E virus (HEV): strain variation in the nonstructural gene region e

A:Reference number: A48547; MUID:92271462

A:Accession: B48547

A:Molecule type: genomic RNA

A:Residues: 965-1691 <FHY>

A>Note: sequence extracted from NCBI backbone (NCBIN:104576, NCBIP:104578)

C:Superfamily: hepatitis E virus nonstructural protein

C:Keywords: ATP; GTP binding; nonstructural protein; nucleotide binding; nucleotidylt

F:973-980/Region: nucleotide-binding motif A (P-loop)

F:979/Binding site: ATP/GTP (Lys) #status predicted

Query Match 5.4%; Score 8; DB 1; Length 1691;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 LAEELGHR 116

Db 1243 LAEELGHR 1250

```
RESULT 9
NMNWME
genome polyprotein - hepatitis E virus (strain Burma)
N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: hepatitis E virus
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-Jul-1999
C:Accession: A40778; A48547
R:Ram, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.
Virology 185, 120-131, 1991
A:Title: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vi
A:Reference number: A40778; MUID:92024067
A:Accession: A40778
A:Molecule type: genomic RNA
A:Residues: 1-1693 <TAM>
A:Cross-references: GB:M73218; NID:9330023; PIDN:AAA45734.1; PID:9330024
R:Fry, K.E.; Tam, A.W.; Smith, M.M.; Kim, J.P.; Luk, K.C.; Young, L.M.; Pistak, M.; Feld
Virus Genes 6, 173-185, 1992
A:Title: Hepatitis E virus (HEV): strain variation in the nonstructural gene region enc
Reference number: A48547; MUID:92271462
C:Accession: A48547
Molecule type: genomic RNA
A:Residues: 967-1693 <FRY>
A:Cross-references: GB:M32400; NID:9330021; PIDN:AAA03206.1; PID:9330022
A:Note: sequence extracted from NCBI backbone (NCBIN:104572, NCBIPI:104573)
C:Superfamily: hepatitis E virus nonstructural protein
C:Keywords: ATP; nonstructural protein; nucleotidyltransferase

Query Match 5.4%; Score 8; DB 1; Length 1693;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 LAEELGHR 116
DB 1245 LAEELGHR 1252

RESULT 10
AD1515
hypothetical protein lin0660 [imported] - Listeria innocua (strain Clp11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD1515
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussutget, O.; Entlan, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ma
C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1515
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <GIA>
A:Cross-references: GB:AL592022; PIDN:CAC95892.1; PID:g16413100; GSPDB:GN00178
C:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin0660

Query Match 4.7%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 DLAEELG 114
DB 52 DLAEELG 58

RESULT 11
AI115
hypothetical protein lmo0657 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AI1156
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussutget, O.; Entlan, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AI1156
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <GIA>
A:Cross-references: GB:NC_003210; PIDN:CAC98735.1; PID:g16410046; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0657

Query Match 4.7%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 DLAEELG 114
DB 52 DLAEELG 58

RESULT 12
AB1892
hypothetical protein alr0683 [imported] - Anabaena sp. (strain PCC 7120)
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AB1892
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-Fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB1892
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAE72641.1; PID:g17130029; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr0683

Query Match 4.7%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 LAEELGH 115
DB 105 LAEELGH 111

RESULT 13
B72683
hypothetical protein APE0883 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C:Accession: B72683
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
A:Reference number: A72450; MUID:99310339
```

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Query Match 4.7%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 DLAEELG 114
DB 52 DLAEELG 58

RESULT 11
AI115
hypothetical protein lmo0657 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AI1156
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussutget, O.; Entlan, K.D.; Fsihi,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AI1156
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <GIA>
A:Cross-references: GB:NC_003210; PIDN:CAC98735.1; PID:g16410046; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0657

Query Match 4.7%; Score 7; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 DLAEELG 114
DB 52 DLAEELG 58

RESULT 12
AB1892
hypothetical protein alr0683 [imported] - Anabaena sp. (strain PCC 7120)
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AB1892
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-Fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB1892
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAE72641.1; PID:g17130029; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr0683

Query Match 4.7%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 LAEELGH 115
DB 105 LAEELGH 111

RESULT 13
B72683
hypothetical protein APE0883 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C:Accession: B72683
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
A:Reference number: A72450; MUID:99310339
```



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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:28:57 ; Search time 11.94 Seconds

(without alignments)  
479,941 Million cell updates/sec

Title: US-09-016-869b-35

Perfect score: 148  
Sequence: 1 MEPSADMLATAAARGVEEV.....TRGSNHRIDAECPSDIDP 148

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

W size: 0  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : SwissProt\_40:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	81.8	156	1	CDN2_HUMAN
2	72	48.6	138	1	CDN5_HUMAN
3	48	32.4	130	1	CDN5_MOUSE
4	36	24.3	130	1	CDN5_RAT
5	19	12.8	167	1	CDN2_MOUSE
6	14	9.5	171	1	CDN2_MONDO
7	8	5.4	747	1	V222_FOWPY
8	5.4	5.4	1691	1	POLN_HEVME
9	5.4	5.4	1693	1	POLN_HEVBU
10	5.4	5.4	1693	1	POLN_HEVMT
11	5.4	5.4	1693	1	POLN_HEVPA
12	5.4	5.4	166	1	CDN7_HUMAN
13	4.7	4.7	166	1	CDN7_MOUSE
14	4.7	4.7	218	1	GPH_RHOSH
15	4.7	4.7	231	1	MTN_BACSV
16	4.7	4.7	253	1	ADH1_DROHI
17	4.7	4.7	253	1	ADH1_DROMT
18	4.7	4.7	253	1	ADH1_DROMU
19	4.7	4.7	253	1	ADH1_DRONA
20	4.7	4.7	253	1	ADH2_DROHA
21	4.7	4.7	253	1	ADH2_DROHU
22	4.7	4.7	253	1	ADH2_DROHI
23	4.7	4.7	253	1	ADH2_DROMO
24	4.7	4.7	253	1	ADH2_DROMU
25	4.7	4.7	253	1	ADH2_DROMH
26	4.7	4.7	253	1	ADH_DROAD
27	4.7	4.7	253	1	ADH_DROAF
28	4.7	4.7	253	1	ADH_DRODI
29	4.7	4.7	253	1	ADH_DROGR
30	4.7	4.7	253	1	ADH_DROHA
31	4.7	4.7	253	1	ADH_DROHE
32	4.7	4.7	253	1	ADH_DROMM
33	4.7	4.7	253	1	ADH_DROMH

34	7	4.7	253	1	ADH_DROHI	000672 drosophila
35	7	4.7	253	1	ADH_DROPI	P23361 drosophila
36	7	4.7	253	1	ADH_DROPL	P23277 drosophila
37	7	4.7	253	1	ADH_DROSL	P23278 drosophila
38	7	4.7	254	1	ADH_DROLE	P10807 drosophila
39	7	4.7	295	1	MYRA_MTCGR	P37000 micromosp
40	7	4.7	348	1	ADH2_CANAL	094038 candida alb
41	7	4.7	364	1	YH31_MTCUT	Q10503 mycobacteri
42	7	4.7	466	1	VP19_HSV2H	P22486 herpes simp
43	7	4.7	466	1	VP19_HSV2H	P89461 herpes simp
44	7	4.7	523	1	PUR9_MTCUT	P71553 m bifunctio
45	7	4.7	527	1	SEUB_SERMA	P21409 serrata ma
46	7	4.7	535	1	Y897_MTCUT	Q10555 mycobacteri
47	7	4.7	575	1	PT1_ECOLI	P08839 escherichia
48	7	4.7	575	1	PT1_SALTY	P12654 salmonella
49	7	4.7	612	1	YC81_MTCUT	Q11040 mycobacteri
50	7	4.7	676	1	CMC2_MOUSE	099xx4 mus musculi
51	7	4.7	700	1	UVRD_MTCUT	053344 mycobacteri
52	7	4.7	706	1	UL17_HSVB	P28950 equine herp
53	7	4.7	889	1	C122_HUMAN	Q9b2q6 homo sapien
54	7	4.7	1880	1	ANK1_HUMAN	P16157 homo sapien
55	7	4.7	2194	1	GLSN_MEPSA	Q03460 medicago sa
56	7	4.7	2397	1	MOKB_SCHPO	Q09854 schizosacch
57	6	4.1	102	1	CH15_DROGR	P13425 drosophila
58	6	4.1	116	1	F411_ADEP2	P36708 human adeno
59	6	4.1	120	1	R18E_AERPE	Q9y551 aeropyrum p
60	6	4.1	122	1	FOLB_ECOLI	P31055 escherichia
61	6	4.1	123	1	ATPE_STRLI	P50011 streptomyce
62	6	4.1	124	1	SGP2_CHRVI	052179 chromatium
63	6	4.1	126	1	TYRT_STPAL	P55046 streptomyce
64	6	4.1	128	1	CAL1_HUMAN	P06881 homo sapien
65	6	4.1	129	1	RS9_BACSV	P21470 bacillus su
66	6	4.1	130	1	RS9_STAM	Q99552 staphylococ
67	6	4.1	130	1	TRJ5_ECOLI	P17907 escherichia
68	6	4.1	137	1	YCE3_HUMAN	Q9y3e2 homo sapien
69	6	4.1	140	1	R1NA_BPPIA	Q03182 bacteriophag
70	6	4.1	141	1	CALO_HUMAN	P01258 homo sapien
71	6	4.1	141	1	HBA_CICCI	P01983 ciconia cic
72	6	4.1	142	1	UP12_ECOLI	P39177 escherichia
73	6	4.1	145	1	Y074_BACAN	Q9rmw0 bacillus an
74	6	4.1	146	1	HBB_CHEKU	P80271 cheilodonic
75	6	4.1	147	1	NIRG_PSEST	Q05254 pseudomonas

## ALIGNMENTS

RESULT 1  
ID CDN2\_HUMAN STANDARD: PRT: 156 AA.  
AC P42771; Q15191;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Cyclin-dependent kinase 4 inhibitor A (CDK4I) (P16-INK4) (P16-INK4A)  
DE (Multiple tumor suppressor 1) (MTS1).  
GN CDKN2A OR CDKN2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94081956; Pubmed=8259215;  
RA Serrano M., Hannon G.J., Beach D.;  
RT "A new regulatory motif in cell-cycle control causing specific  
inhibition of cyclin D/CDK4.";  
RL Nature 366:704-707(1993).  
[2]  
RP SEQUENCE OF 51-152 FROM N.A.  
RX MEDLINE=94204645; Pubmed=8153634;  
RA Kamb A., Grus N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,  
Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,

RA Skolnick M.H.;  
 RT "A cell cycle regulator potentially involved in genesis of many tumor  
 RT types."; Science 264:436-440(1994).  
 RL [3]  
 RP SEQUENCE OF 1-20 FROM N.A.  
 RX MEDLINE=9618208; PubMed=8622687;  
 RA Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;  
 RT "Regulation of p16CDKN2 expression and its implications for cell  
 RT immortalization and senescence."; Mol. Cell. Biol. 16:859-867(1996).  
 RL [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.  
 RX MEDLINE=98421670; PubMed=9751050;  
 RA Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;  
 RT "Structural basis for inhibition of the cyclin-dependent kinase Cdk6  
 RT by the tumour suppressor p16INK4a."; Nature 395:237-243(1998).  
 RL [5]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=20027100; PubMed=10559205;  
 RA Yuan C., Li J., Selby T.L., Byeon I.J., Tsai M.D.;  
 RT "Tumor suppressor INK4: comparisons of conformational properties  
 RT between p16(INK4a) and p18(INK4C)."; J. Mol. Biol. 294:201-211(1999).  
 RL [6]  
 RP REVIEW ON MELANOMA VARIANTS.  
 RX MEDLINE=96377761; PubMed=8783570;  
 RA Dracopoli N.C., Fountain J.W.;  
 RT "CDKN2 mutations in melanoma."; Cancer Surv. 26:115-132(1996).  
 RL [7]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=96303699; PubMed=8723678;  
 RA Smith-Soerensen B., Hoyig E.;  
 RT "CDKN2A (p16INK4A) somatic and germline mutations."; Hum. Mutat. 7:294-303(1996).  
 RL [8]  
 RP VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).  
 RX MEDLINE=94338359; PubMed=860323;  
 RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;  
 RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41  
 RT (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small  
 RT cell lung carcinomas."; Biochem. Biophys. Res. Commun. 202:1426-1430(1994).  
 RL [9]  
 RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 AND  
 RP THR-148.  
 RX MEDLINE=95078916; PubMed=7987387;  
 RA Hussussian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,  
 RT Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;  
 RT "Germline p16 mutations in familial melanoma."; Nat. Genet. 8:15-21(1994).  
 RL [10]  
 RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.  
 RX MEDLINE=95060835; PubMed=7970734;  
 RA Zhou X., Tarmim L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,  
 RT Abraham J.M., Meltzer S.J.;  
 RT "The MTS1 gene is frequently mutated in primary human esophageal  
 RT tumors."; Oncogene 9:3737-3741(1994).  
 RL [11]  
 RP VARIANTS.  
 RX MEDLINE=95188190; PubMed=7882351;  
 RA Okamoto A., Hussain S.P., Hagiwara K., Spillare F.A., Rusin M.R.,  
 RA Demetrick D.J., Serrano M., Hannon G.J., Shisaki M., Zaitzala M.,  
 RA Bennett W.P., Forester K., Gerwin B., Beach D.H., Harris C.C.;  
 RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 gene in  
 RT primary and metastatic lung cancer."; Cancer Res. 55:1448-1451(1995).  
 RL [12]  
 RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.  
 RX MEDLINE=96121580; PubMed=8595405;

RA Walker G.J., Hussussian C.J., Flores J.F., Glendenning J.M.,  
 RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;  
 RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma  
 RT kindreds."; Hum. Mol. Genet. 4:1845-1852(1995).  
 RL [13]  
 RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 AND  
 RP T-148.  
 RX MEDLINE=95375774; PubMed=7647780;  
 RA Radeke K., Hussussian C.J., Sikorski R.S., Varmus H.E.,  
 RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.D., Beach D.,  
 RA Dracopoli N.C.;  
 RT "Mutations associated with familial melanoma impair p16INK4  
 RT function."; Nat. Genet. 10:114-116(1995).  
 RL [14]  
 RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.  
 RX MEDLINE=96333259; PubMed=8710906;  
 RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., MacDonald D.J.,  
 RA Luchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,  
 RA Isselbacher K.J., Sober A.J., Haber D.A.;  
 RT "Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in  
 RT familial melanoma: analysis of a clinic-based population."; Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).  
 RL [15]  
 RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.  
 RX MEDLINE=97472457; PubMed=9328469;  
 RA Harland M., Meloni R., Guis N., Pinney E., Brookes S., Spurr N.K.,  
 RA Fritschau A.-M., Bataille V., Peters G., Cuzick J., Selby P.,  
 RA Bishop D.T., Bishop J.N.;  
 RT "Germline mutations of the CDKN2 gene in UK melanoma families."; Hum. Mol. Genet. 6:2061-2067(1997).  
 RL [16]  
 RP VARIANTS FAMILIAL MELANOMA.  
 RX MEDLINE=96087572; PubMed=9425228;  
 RA Soufir N., Avril M.-F., Chompret A., Demeunais F., Bombléd J.,  
 RA Spatz A., Stoppa-Lyonnet D., Bernard J., Bressac-De Pallierets B.;  
 RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone  
 RT families in France."; Hum. Mol. Genet. 7:209-216(1998).  
 RL [17]  
 RP ERRATUM.  
 RA Soufir N., Avril M.-F., Chompret A., Demeunais F., Bombléd J.,  
 RA Spatz A., Stoppa-Lyonnet D., Bernard J., Bressac-De Pallierets B.;  
 RT Hum. Mol. Genet. 7:941-941(1998).  
 RL [18]  
 RP VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.  
 RA Gretsdoctir S., Olafsdottir G.H., Borg A.;  
 RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,  
 RT glioma and carcinoma of the pancreas."; Hum. Mutat. 12:212-212(1998).  
 RL [19]  
 RP VARIANTS MELANOMA GLY-59; TYR-84; TRP-87 AND TRP-101.  
 RX MEDLINE=20332815; PubMed=10874641;  
 RA Ruiz A., Puig S., Malveyh J., Lazaro C., Lynch M., Gimenez-Arnau A.M.,  
 RA Puig L., Sanchez-Conejo J., Estivill X., Castel T.;  
 RT "CDKN2A mutations in Spanish cutaneous malignant melanoma families and  
 RT patients with multiple melanomas and other neoplasia."; J. Med. Genet. 36:490-493(1999).  
 RL -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS  
 CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE  
 CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.  
 CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.  
 CC -1- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A  
 CC WIDE RANGE OF TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 CC INHIBITORS.  
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.  
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CC -----  
 DR EMBL: L27211; AAA92554.1; -  
 DR EMBL: U12820; AAB60645.1; -  
 DR EMBL: U12818; AAB60645.1; JOINED.  
 DR EMBL: U12819; AAB60645.1; JOINED.  
 DR EMBL: S69804; AAD14048.1; -  
 DR EMBL: X94154; CAA63870.1; -  
 DR PDB: 1B17; 16-FEB-99.  
 DR PDB: 1DC2; 23-DEC-99.  
 DR MIM: 600160; -  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 3.  
 DR PROSITE: PS50088; ANK\_REPEAT; FALSE\_NEG.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;  
 KW Polymorphism; Li-Fraumeni syndrome; 3D-structure.  
 FT REPEAT 11 40 ANK 1.  
 FT REPEAT 44 72 ANK 2.  
 FT REPEAT 77 106 ANK 3.  
 FT REPEAT 110 139 ANK 4.  
 FT VARIANT 14 14 D -> E (IN A BILIARY TRACT TUMOR).  
 FT VARIANT 16 16 /FTID-VAR\_001408.  
 FT VARIANT 16 16 L -> P (IN A BILIARY TRACT TUMOR AND A  
 FT VARIANT 16 16 FAMILIAL MELANOMA).  
 FT VARIANT 20 20 /FTID-VAR\_001409.  
 FT VARIANT 20 20 A -> P (IN A LUNG TUMOR AND MELANOMA).  
 FT VARIANT 20 20 /FTID-VAR\_001410.

Query Match 81.8%; Score 121; DB 1; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 2e-110;  
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QY 28 ALPNAANSNGRRPIQVMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLV 87  
 DB 36 ALPNAANSNGRRPIQVMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95  
 DB 88 VLHRAAGARDVDAMGRLLPVDLAEEIGHRDVARYLAAAGTRGSHARIDAEEPSDIP 147  
 DB 96 VLHRAAGARDVDAMGRLLPVDLAEEIGHRDVARYLAAAGTRGSHARIDAAREGSPDIP 155

QY 148 D 148  
 DB 156 D 156

CC  
 ID 2  
 CDNS\_HUMAN STANDARD; PRT; 138 AA.  
 AC P42772;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cyclin-dependent kinase 4 inhibitor B (P15-INK4B) (P15-INK4B)  
 DE (Multiple tumor suppressor 2) (MTS2).  
 GN CDKN2B OR MTS2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCB1\_TaxID=9606;  
 RX NCB1\_TaxID=9606;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95095079; PubMed=8001816;  
 RA Guan K.-T., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,  
 RA Matera G.A., Xiong Y.,  
 RT "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related  
 RT CDK4 inhibitor, correlates with wild-type p18 function."  
 RL Genes Dev. 8:2939-2952(1994).  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94359613; PubMed=8078588;

RA Hannon G.J., Beach D.  
 RT "p15INK4B is a potential effector of TGF-beta-induced cell cycle  
 RT arrest."  
 RL Nature 371:257-261(1994).  
 RN 13  
 RP SEQUENCE OF 53-138 FROM N.A.  
 RX MEDLINE=94204645; PubMed=8153634;  
 RA Kamb A., Gruts N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,  
 RA Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,  
 RA Skolnick M.H.;  
 RT "A cell cycle regulator potentially involved in genesis of many tumor  
 RT types."  
 RL Science 264:436-440(1994).  
 RN 14  
 RP VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50.  
 RX MEDLINE=95188190; PubMed=7882351;  
 RA Okemoto A., Hussain S.P., Hagihara K., Spillare E.A., Rusin M.R.,  
 RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zarwala M.,  
 RA Xiong Y., Beach D.H., Yokota J., Harris C.C.,  
 RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in  
 RT primary and metastatic lung cancer."  
 RL Cancer Res. 55:1448-1451(1995).  
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6, POTENT INHIBITOR.  
 CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.  
 CC -1- DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.  
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 CC INHIBITORS.  
 CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.

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CC -----  
 DR EMBL: U17075; AAC50075.1; -  
 DR EMBL: L36844; AAA50282.1; -  
 DR EMBL: S69805; AAD14049.1; -  
 DR HSP: P42771; 1B17.  
 DR MIM: 600431; -  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 3.  
 DR PROSITE: PS50088; ANK\_REPEAT; FALSE\_NEG.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation.  
 FT REPEAT 13 39 ANK 1 (INCOMPLETE).  
 FT REPEAT 73 103 ANK 2.  
 FT VARIANT 47 47 G -> E (IN LUNG ADENOCARCINOMA).  
 FT VARIANT 50 50 /FTID-VAR\_001488.  
 FT VARIANT 50 50 A -> V (IN LUNG ADENOCARCINOMA).  
 FT VARIANT 50 50 /FTID-VAR\_001489.  
 FT VARIANT 50 50 SA -> TP (IN REF. 2).  
 FT CONFLICT 20 21 MISSING (IN REF. 2).  
 FT CONFLICT 23 23 MISSING (IN REF. 2).  
 FT CONFLICT 32 34 QLL -> HSW (IN REF. 2).  
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Query Match 48.6%; Score 72; DB 1; Length 138;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-63;  
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IQVMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARDVD 100  
 DB 51 IQVMMGSAVAELLHLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARDVD 110  
 QY 101 AMGRLPVDLAE 112  
 DB 111 AMGRLPVDLAE 122

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RESULT 3
CDN5_MOUSE STANDARD: PRT; 130 AA.
ID AC P55271;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95380169; PubMed=7651726;
RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.,
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes."
RT Oncogene 11:635-643(1995).
[2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J X DBA;
RX MEDLINE=97322242; PubMed=9178896;
RA Malumbres M., de Castro I., Santos J., Melendez B., Manques R.,
RA Serrano M., Pellicer A., Fernandez-Piqueras J.,
RT "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by
RT deletion and de novo methylation with independence of p16INK4a
RT alterations in murine primary T-cell lymphomas."
RT Oncogene 14:1361-1370(1997).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED UBQUITOUSLY.
CC -1- INDUCTION: BY TGF-BETA.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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CC -----
CC EMBL: U66085; AAB39833.1; -.
CC EMBL: U66084; AAB39833.1; JOINED.
CC HSSP: P42771; 1B7.
DR MGD: MGI:104737; Cdkn2b.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 3.
DR SMART: SM00248; ANK; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat.
FT REPEAT 5 34 ANK 1.
FT REPEAT 38 66 ANK 2.
FT REPEAT 71 100 ANK 3.
FT REPEAT 104 130 ANK 4.
FT REPEAT 130 130 ANK 4.
SO SEQUENCE 130 AA; 13788 MW; 7AAD60FF552BCF9 CRC64;

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Query Match 32.4%; Score 48; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 1,7e-39;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 51 VAEILLHGAEPCADPATLTRPVHDAAREGFLDTLVLRHAGARLDV 98
DB 53 VAEILLHGAEPCADPATLTRPVHDAAREGFLDTLVLRHAGARLDV 100

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RESULT 4
CDN5_RAT STANDARD: PRT; 130 AA.
ID AC P55272;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cyclin-dependent kinase 4 inhibitor B (P14-INK4B) (P15-INK4B).
GN CDKN2B OR INK4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96001392; PubMed=7546221;
RA Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y.,
RA Tsuchiya H., Kikuchi Y., Mitani H.,
RT "Molecular genetic basis of renal carcinogenesis in the Eker rat
RT model of tuberosus sclerosis (Tsc2).";
RT Mol. Carcinog. 14:23-27(1995).
[2]
SEQUENCE OF 46-86 FROM N.A.
RX MEDLINE=95228036; PubMed=7712460;
RA Knapek D.F., Serrano M., Beach D., Trono D., Walker C.L.,
RT "Association of rat p15INK4b/p16INK4 deletions with monosomy 5 in
RT kidney epithelial cell lines but not primary renal tumors."
RT Cancer Res. 55:1607-1612(1995).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
CC SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN
CC TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL
CC KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: S79760; AAB35360.1; -.
CC EMBL: S77734; -. NOT_ANNOTATED_CDS.
DR HSSP: O60773; 1A7.
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 3.
DR SMART: SM00248; ANK; 1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
FT CHAIN 1 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT LONG ISOFORM.
FT CHAIN 46 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT INIT MET 46 46 SHORT ISOFORM.
FT REPEAT 5 34 ANK 1.
FT REPEAT 38 66 ANK 2.
FT REPEAT 71 100 ANK 3.
FT REPEAT 104 130 ANK 4.
SO SEQUENCE 130 AA; 13748 MW; AC45B21FA69FAD92 CRC64;

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Query Match 24.3%; Score 36; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 7.8e-28;

```

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VAEILLHGAEPNCADPATLTPVHDAREGFLDTL 86  
Db 53 VAEILLHGAEPNCADPATLTPVHDAREGFLDTL 88

RESULT 5  
ID CDN2\_MOUSE STANDARD; PRT; 167 AA.  
AC P51480;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Cyclin-dependent kinase 4 inhibitor A (CDK4I) (P16-INK4) (P16-INK4A).  
GN CDKN2A OR P16INK4A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RA SEQUENCE FROM N.A.  
RX MEDLINE=95380169; Pubmed=7651726;  
RA Quail D.E., Asmann R.A., Hannon G.J., Rehberger P.A., Trono D., Richter K.H., Walker C., Beach D., Sherr C.J., Seriano M., "Cloning and characterization of murine p16INK4a and p15INK4b genes."; Oncogene 11:635-645(1995).  
RT -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6.  
CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES  
CC -1- CONTAINED CDK6.  
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.  
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.  
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.  
CC -----  
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CC -----  
DR EMBL; L76150; AAA85453.1; -  
DR HSSP; Q60773; 1AP7.  
DR MGDP; MGI:104738; Cdkn2a.  
DR InterPro: IPR002110; ANK.  
DR Pfam: PF00023; ank; 3.  
DR SMART; SM00248; ANK; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; FALSE\_NEG.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KM Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.  
FT CHAIN 1 167 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT LONG ISOFORM.  
FT CHAIN 43 167 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT INIT\_MET 43 43 SHORT ISOFORM.  
FT REPEAT 35 63 FOR SHORT ISOFORM.  
FT REPEAT 101 130 ANK 1.  
FT REPEAT 167 17870 ANK 2.  
SQ SEQUENCE 167 AA; 17870 MW; 88C458BA105ECB8F CRC64;

Query Match 12.8%; Score 19; DB 1; Length 167;  
Best Local Similarity 100.0%; Pred. No. 3.3e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPVHDAREGFLDTLVYLH 90  
Db 71 RPVHDAREGFLDTLVYLH 89

RESULT 6  
ID CDN2\_MONDO STANDARD; PRT; 171 AA.  
AC 077617;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Cyclin-dependent kinase 4 inhibitor A (CDK4I) (P16-INK4) (P16-INK4A) (Tumor suppressor CDKN2A).  
GN CDKN2A.  
OS Monodelphis domestica (Short-tailed grey opossum).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.  
OX NCBI\_TaxID=13616;  
RA SEQUENCE FROM N.A.  
RX Sherburn T.E., Gale J.M., Ley R.D.; Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RL -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).  
CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).  
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.  
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE INHIBITORS.  
CC -1- SIMILARITY: CONTAINS 3 ANK REPEATS.  
CC -----  
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CC -----  
DR EMBL; AF064808; AAC23669.1; -  
DR EMBL; AF064808; AAC23670.1; -  
DR HSSP; P42771; 1B17.  
DR InterPro: IPR002110; ANK.  
DR Pfam; PF00023; ank; 3.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
KM Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.  
FT CHAIN 1 171 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT LONG ISOFORM.  
FT CHAIN 35 171 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,  
FT INIT\_MET 35 35 SHORT ISOFORM.  
FT REPEAT 45 74 FOR SHORT ISOFORM.  
FT REPEAT 78 106 ANK 1.  
FT REPEAT 111 140 ANK 2.  
FT REPEAT 171 18707 ANK 3.  
SQ SEQUENCE 171 AA; 18707 MW; 694264F5D0F4F6CC CRC64;

Query Match 9.5%; Score 14; DB 1; Length 171;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 PVHDAREGFLDTL 86  
Db 115 PVHDAREGFLDTL 128

RESULT 7  
V222\_F0WV STANDARD; PRT; 747 AA.  
AC Q9J513;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Putative ankyrin-repeat protein FPV222.  
GN FPV222.  
OS Fowlpox virus (FPV)  
OC Viruses; dsDNA viruses, no RNA stage: Poxviridae; Chordopoxvirinae;  
OC Avipoxvirus.  
OX NCBI\_TaxID=10261;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20193820; PubMed=10729156;  
RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;  
RT "The genome of fowlpox virus."  
J. Virol. 74:3815-3831(2000).  
CC -1- SIMILARITY: CONTAINS 14 ANK REPEATS.  
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DR EMBL: AF198100; AAF44566.1; -  
DR InterPro: IPR002110; ANK.  
DR Pfam: PF00023; ank; 12.  
DR SMART: SM00248; ANK; 9.  
DR PROSITE: PS50088; ANK\_REPEAT: 7.  
DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
DR PROSITE: PS50088; ANK\_REPEAT; 1.  
KW Hypothetical protein; Repeat; ANK repeat.  
FT REPEAT 38 67  
FT REPEAT 103 132 ANK 1.  
FT REPEAT 136 165 ANK 2.  
FT REPEAT 169 198 ANK 3.  
FT REPEAT 202 231 ANK 4.  
FT REPEAT 224 263 ANK 5.  
FT REPEAT 234 263 ANK 6.  
FT REPEAT 328 357 ANK 7.  
FT REPEAT 361 393 ANK 8.  
FT REPEAT 397 426 ANK 9.  
FT REPEAT 430 460 ANK 10.  
FT REPEAT 464 493 ANK 11.  
FT REPEAT 495 524 ANK 12.  
FT REPEAT 529 559 ANK 13.  
FT REPEAT 559 593 ANK 14.  
SQ SEQUENCE 747 AA; 85303 MW; 55F90AF2855C3D28 CRC64;

Query Match 5.4%; Score 8; DB 1; Length 747;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 53 ELLIHGA 60  
|||||||  
DB 154 ELLIHGA 161

RESULT 8  
POLN\_HEVME STANDARD; PRT: 1691 AA.  
AC 003495;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Non-structural polyprotein [Contains: RNA-directed RNA polymerase  
DE (EC 2.7.7.48); Helicase].  
OS Hepatitis E virus (strain Mexico) (HEV).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage.  
OX NCBI\_TaxID=31768;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93079857; PubMed=1448913;  
RA Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E.,  
RA Bradley D.W., Tam A.W., Reyes G.R.;  
RT "Molecular cloning and sequencing of the Mexico isolate of hepatitis

RT E virus (HEV)."  
RN Virology 191:550-558(1992).  
RN [2]  
RP SEQUENCE OF 965-1691 FROM N.A.  
RX MEDLINE=92271462; PubMed=1569964;  
RA Fry K.E., Tam A.W., Smith M.M., Kim J.P., Luk K.C., Young L.M.,  
RA Platack M., Feldman R.A., Yun K.Y., Pundy M.A., McCaustland K.A.,  
RA Bradley D.W., Reyes G.R.;  
RT "Hepatitis E virus (HEV): strain variation in the nonstructural gene  
RT region encoding consensus motifs for an RNA-dependent RNA polymerase  
RT and an ATP/GTP binding site."  
J. Virol. 74:173-185(1992).  
CC -1- MISCELLANEOUS: HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF  
CC ENTERICALLY TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).  
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CC EMBL: M74506; AAA5730.1; -  
DR PIR: A44212; A44212.  
DR MEROPS: C41.001; -  
DR InterPro: IPR002589; Alpp.  
DR InterPro: IPR002588; RNA\_dep\_RNAPol2.  
DR InterPro: IPR002588; V\_methyltransf.  
DR InterPro: IPR000606; Viral\_helicase.  
DR Pfam: PF01661; Alpp; 1.  
DR Pfam: PF00978; RNA\_dep\_RNAPol2; 1.  
DR Pfam: PF01443; Viral\_helicase; 1.  
DR Pfam: PF01660; Vmethyltransf; 1.  
DR SMART: SM00506; Alpp; 1.  
KW Polyprotein; Transferase; RNA-directed RNA polymerase; Helicase;  
KW ATP-binding.  
FT NP\_BIND 973 980 ATP (POTENTIAL).  
SQ SEQUENCE 1691 AA; 185224 MW; DB3F0B2C913F871B CRC64;

Query Match 5.4%; Score 8; DB 1; Length 1691;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 109 LAELGHR 116  
|||||||  
DB 1243 LAELGHR 1250

RESULT 9  
POLN\_HEVBU STANDARD; PRT: 1693 AA.  
AC P29324;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Non-structural polyprotein [Contains: RNA-directed RNA polymerase  
DE (EC 2.7.7.48); Helicase].  
OS Hepatitis E virus (strain Burma) (HEV).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage.  
OX NCBI\_TaxID=31767;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92024067; PubMed=1926770;  
RA Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,  
RA Fry K.E., Reyes G.R.;  
RT "Hepatitis E virus (HEV): molecular cloning and sequencing of the  
RT full-length viral genome."  
J. Virology 185:120-131(1991).  
CC -1- MISCELLANEOUS: HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF  
CC ENTERICALLY TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).  
-----

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 19, 2002, 17:28:37 ; Search time 26.76 Seconds

(without alignments)  
956.773 Million cell updates/sec

Title: US-09-016-869B-35

Perfect score: 148

Sequence: 1 MESPADWLATRAARGVEEV.....TRGSNARIDAEGPSDIPD 148

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Wt size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database : SPTREMBL.19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	71.6	106	4 Q9NP05	Q9NP05 homo sapien
2	54	36.5	81	6 Q9GMF2	Q9GMF2 canis faml
3	51	34.5	86	6 Q9XS52	Q9XS52 felis silve
4	51	34.5	102	6 Q9XS51	Q9XS51 felis silve
5	48	32.4	86	11 Q9QUP0	Q9QUP0 mus musculu
6	48	32.4	86	11 Q94846	Q94846 mus musculu
7	48	32.4	86	11 Q9Z1C1	Q9Z1C1 mus scrofa
8	47	31.8	103	6 Q9TXY1	Q9TXY1 mus scrofa
9	32	21.6	130	11 Q91YF9	Q91YF9 mesocricetu
10	26	17.6	36	4 Q9UPB7	Q9UPB7 homo sapien
11	26	17.6	86	6 Q9TXY0	Q9TXY0 sus scrofa
12	26	17.6	116	4 Q95440	Q95440 homo sapien
13	19	12.8	112	11 Q9QWH4	Q9QWH4 mus musculu
14	19	12.8	113	11 Q9Z1C2	Q9Z1C2 mus musculu
15	19	12.8	159	11 Q9R023	Q9R023 ratu mus norv
16	19	12.8	168	11 Q9R088	Q9R088 mus musculu

17	19	12.8	168	11 Q97510	Q97510 mus musculu
18	18	12.2	113	11 Q9QWH8	Q9QWH8 mus musculu
19	18	12.2	113	11 Q9QWH7	Q9QWH7 mus musculu
20	18	12.2	113	11 Q9QWH6	Q9QWH6 mus musculu
21	15	10.1	58	6 Q97886	Q97886 equus cabal
22	15	10.1	113	11 Q9QWH5	Q9QWH5 mus musculu
23	14	9.5	21	4 Q9UD00	Q9UD00 homo sapien
24	12	8.1	144	11 Q99PH0	Q99PH0 mesocricetu
25	12	8.1	157	11 Q9EQ33	Q9EQ33 mesocricetu
26	5.4	4.4	11	Q9OUJ3	Q9OUJ3 mus musculu
27	5.4	4.4	11	Q9Z1C0	Q9Z1C0 mus musculu
28	5.4	4.4	91	12 Q9W1J9	Q9W1J9 hepatitis e
29	5.4	4.4	124	13 Q9W618	Q9W618 xiphophorus
30	5.4	4.4	300	12 P70067	P70067 xiphophorus
31	5.4	4.4	300	12 P89468	P89468 herpes simp
32	5.4	4.4	303	16 Q92NR2	Q92NR2 rhizobium m
33	5.4	4.4	334	17 Q92818	Q92818 archaeoglob
34	5.4	4.4	390	3 Q94237	Q94237 schizosacch
35	5.4	4.4	487	12 Q91869	Q91869 hepatitis e
36	5.4	4.4	544	2 Q9AG77	Q9AG77 streptomyce
37	5.4	4.4	727	12 Q91873	Q91873 hepatitis e
38	5.4	4.4	1050	4 Q9H014	Q9H014 homo sapien
39	5.4	4.4	1060	4 Q96NM4	Q96NM4 homo sapien
40	5.4	4.4	1205	3 Q9HFR5	Q9HFR5 schizosacch
41	5.4	4.4	1685	12 Q9E8G6	Q9E8G6 hepatitis e
42	5.4	4.4	1693	12 Q98444	Q98444 hepatitis e
43	5.4	4.4	1693	12 Q91862	Q91862 hepatitis e
44	5.4	4.4	1693	12 Q91344	Q91344 hepatitis e
45	5.4	4.4	1693	12 Q96410	Q96410 hepatitis e
46	5.4	4.4	1693	12 Q93921	Q93921 hepatitis e
47	5.4	4.4	1693	12 Q9W1L5	Q9W1L5 hepatitis e
48	5.4	4.4	1693	12 Q9WC28	Q9WC28 hepatitis e
49	5.4	4.4	1693	12 Q91876	Q91876 hepatitis e
50	5.4	4.4	1698	12 Q9YLK3	Q9YLK3 hepatitis e
51	5.4	4.4	1703	12 Q91116	Q91116 hepatitis e
52	5.4	4.4	1707	12 Q91Y29	Q91Y29 hepatitis e
53	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 hepatitis e
54	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
55	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
56	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
57	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
58	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
59	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
60	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
61	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
62	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
63	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
64	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
65	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
66	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
67	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
68	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
69	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
70	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
71	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
72	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
73	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
74	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat
75	5.4	4.4	1708	12 Q9YLR1	Q9YLR1 swine hepat

## ALIGNMENTS

RESULT 1  
Q9NP05  
AC Q9NP05; PRELIMINARY; PRT; 106 AA.  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE CDK41 PROTEIN (FRAGMENT).  
GN CDK41.

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94203288; PubMed=8152487;
RX Nobori T., Miura K., Wu D.J., Lois A., Takabayashi K., Carson D.A.;
RT "Deletions of the cyclin-dependent kinase-4 inhibitor gene in multiple
human cancers.";
RL Nature 368:753-756(1994).
DR EMBL; S69824; AAD14050.1; -.
DR EMBL; S69822; AAD14050.1; JOINED.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Repeat.
FT NON_TER 1
SQ SEQUENCE 106 AA; 11314 MW; 2D59442F956B6A61 CRC64;

Query Match
Best Local Similarity 71.6%; Score 106; DB 4; Length 106;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 VMMGSAARVAELLHLGAEPCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDRAM 102
DB 1 VMMGSAARVAELLHLGAEPCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDRAM 60

QY 103 GRLPVDLAELGHRDVARVYRAAGSTRGSNARIDAAEGSPDIP 148
DB 61 GRLPVDLAELGHRDVARVYRAAGSTRGSNARIDAAEGSPDIP 106

RESULT 2
Q9GME2
ID Q9GME2 PRELIMINARY; PRT; 81 AA.
AC Q9GME2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4/6 INHIBITOR-A (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBL_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Venkatrej V.S., Mayor J., Modiano J.F.;
RT "Role of p16/Ink4-a in familial canine cancers.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF234176; AAG01087.1; -.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Kinase; Repeat.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 8868 MW; 0E39D8D805BEAC0F CRC64;

Query Match
Best Local Similarity 36.5%; Score 54; DB 6; Length 81;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 TLTTPVHDAREGFLDTLVVLRAGARLDVDRAMGRLPVDLAEEIGHRDVARYL 122
DB 27 TLTTPVHDAREGFLDTLVVLRAGARLDVDRAMGRLPVDLAEEIGHRDVARYL 80

RESULT 3
Q9XS52
ID Q9XS52 PRELIMINARY; PRT; 86 AA.
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AC Q9XS52;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P15/MTS2/CDKN2B (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBL_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-PERIPHERAL BLOOD;
RC Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
RA Nishigaki K., Matari T., Tsujimoto H., Hasegawa A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010808; BAA33541.1; -.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR Pfam; PF00023; ank; 3.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Repeat.
FT NON_TER 1
FT NON_TER 102
SQ SEQUENCE 102 AA; 10824 MW; 26399FF21359F35D CRC64;

Query Match
Best Local Similarity 34.5%; Score 51; DB 6; Length 86;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 PNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDRAMGRLPVDLAEE 112
DB 20 PNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDRAMGRLPVDLAEE 70

RESULT 4
Q9XS51
ID Q9XS51 PRELIMINARY; PRT; 102 AA.
AC Q9XS51;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P16/CDKN2A/MTS1 (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBL_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-PERIPHERAL BLOOD;
RC Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
RA Nishigaki K., Matari T., Tsujimoto H., Hasegawa A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010807; BAA33540.1; -.
DR HSSP; P42771; 1B17.
DR InterPro: IPR002110; ANK.
DR Pfam; PF00023; ank; 3.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Repeat.
FT NON_TER 1
FT NON_TER 102
SQ SEQUENCE 102 AA; 10824 MW; 26399FF21359F35D CRC64;

Query Match
Best Local Similarity 34.5%; Score 51; DB 6; Length 102;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 PNCADPATLTRPVHDAREGFLDTLVVLRAGARLDVDRAMGRLPVDLAEE 112
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Db 20 PNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVBDANGRLPVDAEE 70

RESULT 5  
ID 090P0 PRELIMINARY; PRT; 86 AA.

AC 090P0; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.  
RC STRAIN-VARIOUS STRAINS;  
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
R. Pellicer A., Fernandez-Piqueras J.;  
RT Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains.";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U79639; AAD00234.1; -;  
DR EMBL; U79638; AAD00232.1; -;  
DR HSSP; P42771; 1B17.  
DR InterPro: IPR002110; ANK.  
DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
KW ANK repeat; Cyclin; Kinase; Repeat.  
FT NON\_TER 1 86  
FT SEQUENCE 86 AA; 9269 MW; 509D9B3613251B18 CRC64;

Query Match 32.4%; Score 48; DB 11; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1,1e-37;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VAEILLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDV 98  
DB 9 VAEILLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDV 56

RESULT 6  
ID 054846 PRELIMINARY; PRT; 86 AA.

AC 054846; 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;

RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6J;  
MDLINE=99124385; PubMed=9927195;  
RA Malumbres M., de Castro I.P., Santos J., Piqueras J.F., Pellicer A.;  
RT "Hypermethylation of the cell cycle inhibitor p15INK4b 3'-untranslated  
region interferes with its transcriptional regulation in primary  
lymphomas.";  
RL Oncogene 18:385-396(1999).  
DR EMBL; AF015460; AAB94534.1; -;  
DR HSSP; P42771; 1B17.  
DR InterPro: IPR002110; ANK.  
DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
KW ANK repeat; Kinase; Repeat.  
FT NON\_TER 1 86

SQ SEQUENCE 86 AA; 9237 MW; 0499DB26144FB6DF CRC64;

Query Match 32.4%; Score 48; DB 11; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1,1e-37;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VAEILLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDV 98  
DB 9 VAEILLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDV 56

RESULT 7  
ID 0921C1 PRELIMINARY; PRT; 86 AA.

AC 0921C1; 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
OS Mus musculus (Western wild mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10096;

RP SEQUENCE FROM N.A.  
RC STRAIN-SPRET/EL;  
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
R. Pellicer A., Fernandez-Piqueras J.;  
RT Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains.";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U79637; AAD00237.1; -;  
DR HSSP; P42771; 1B17.  
DR InterPro: IPR002110; ANK.  
DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
KW ANK repeat; Kinase; Repeat.  
FT NON\_TER 1 86  
FT SEQUENCE 86 AA; 9269 MW; 509D9B3613251B18 CRC64;

Query Match 32.4%; Score 48; DB 11; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1,1e-37;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 VAEILLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDV 98  
DB 9 VAEILLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDV 56

RESULT 8  
ID 09T5Y1 PRELIMINARY; PRT; 103 AA.

AC 09T5Y1; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR, P16 (FRAGMENT).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
NCBI\_TaxID=9823;

RP SEQUENCE FROM N.A.  
RC STRAIN-LARGE WHITE;  
RA Le Chalony C., Hayes H., Frelat G., Geoffroy C.;  
RT "Identification and mapping of swine CDKN2A and CDKN2B exon2  
sequences.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ242787; CAB65454.1; -;

DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 2.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1  
 FT NON\_TER 103  
 SQ SEQUENCE 103 AA; 11023 MW; 5D3ABCC1088DE0B CRC64;

Query Match 31.8%; Score 47; DB 6; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 1.le-36;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 DPATLTRPVHDAREGFLDTLVLRHAGARLDVDRMGRLPDAAEE 112  
 DB 24 DPATLTRPVHDAREGFLDTLVLRHAGARLDVDRMGRLPDAAEE 70

RESULT 9  
 ID Q91YF9 PRELIMINARY; PRT; 130 AA.  
 AC Q91YF9;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE P15INK4B CYCLIN-DEPENDENT KINASE INHIBITOR.  
 GN P15INK4B.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PANCREAS;  
 RA Muscarella P., Ulrich A.B., Casto B.C., Moniaux N., Knobloch T.J.,  
 RA Witte U.A., Melvin S., Pour P.M., Song H., Gold B., Batra S.K.,  
 RA Weghorst C.M.;  
 RT "Homologous deletion of p15INK4b/p16INKA Gene Locus in Syrian Golden  
 RT Hamster Tumor Cell Lines";  
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AJ302037; CAC67498.1; -.  
 KW Kinase; Cyclin.  
 SQ SEQUENCE 130 AA; 13842 MW; 4C04DB3F8C6FP013 CRC64;

Query Match 21.6%; Score 32; DB 11; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 2.le-22;  
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 TLTTRPVHDAREGFLDTLVLRHAGARLDVDR 100  
 DB 71 TLTTRPVHDAREGFLDTLVLRHAGARLDVDR 102

RESULT 10  
 ID Q9UPB7 PRELIMINARY; PRT; 36 AA.  
 AC Q9UPB7;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR 2A (FRAGMENT).  
 GN CDKN2A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Murthy S.K., Demetrick D.J.;  
 RT "Genomic sequence of CDKN2A (p16INK4A) 5' to ORF.";

RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF044170; AAD02319.1; -.  
 KW Kinase.  
 FT NON\_TER 36  
 FT NON\_TER 36  
 SQ SEQUENCE 36 AA; 3672 MW; BC8919D2B4194ECA CRC64;

Query Match 17.6%; Score 26; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.le-17;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEPSADWLATTAARGVEEVALLAA 26  
 DB 9 MEPSADWLATTAARGVEEVALLAA 34

RESULT 11  
 ID Q9TST0 PRELIMINARY; PRT; 86 AA.  
 AC Q9TST0;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).  
 GN CDKN2B.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LARGE WHITE;  
 RA MEDLINE=2029098; PubMed=10828598;  
 RA Le Chalony C., Hayes H., Frelat G., Geffroin C.;  
 RT "Identification and mapping of swine cyclin-dependent kinase inhibitor  
 RT CDKN2A and CDKN2B exon2 sequences";  
 RT CytoGenet. Cell Genet. 86:240-243(2000).  
 DR EMBL; AJ242788; CAB65455.1; -.  
 DR HSSP; P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 2.  
 DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 86 AA; 9286 MW; 16EF7A223293CCF9 CRC64;

Query Match 17.6%; Score 26; DB 6; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-17;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 PNCADPATLTRPVHDAREGFLDTLV 87  
 DB 20 PNCADPATLTRPVHDAREGFLDTLV 45

RESULT 12  
 ID Q95440 PRELIMINARY; PRT; 116 AA.  
 AC Q95440;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR P12.  
 GN P16INK4A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PANCREAS;  
 RX MEDLINE=99373016; PubMed=10445844;

RA Robertson K.D., Jones P.A.;  
 RT "Tissue-specific alternative splicing in the human INK4a/ARF cell  
 cycle regulatory locus."  
 RL Oncogene 18:3810-3820(1999).  
 DR EMBL: AF115544; AAD11437.1; -  
 DR InterPro: IPR002110; ANK  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 SQ SEQUENCE 116 AA; 12212 MW; F44DBC80EB3A7C8 CRC64;

Query Match 17.6%; Score 26; DB 4; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MESPADWLATAARGVEYRALLEA 26  
 DB 9 MESPADWLATAARGVEYRALLEA 34  
 |||

RESULT 13  
 ID 090WH4 PRELIMINARY; PRT; 112 AA.  
 AC 090WH4;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
 GN p16(INK4a).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MUS POSCHIAVINUS;  
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
 RA Pellicer A., Fernandez-Piqueras J.;  
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
 in mouse inbred strains."  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U79635; AAD00231.1; -  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 DR ANK repeat; Kinase; Repeat.  
 KW NON\_TER 1  
 FT NON\_TER 112 112  
 SQ SEQUENCE 112 AA; 11956 MW; 65C46A849D0CB65F CRC64;

Query Match 12.8%; Score 19; DB 11; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 RPVHDAREGFLDTLVVH 90  
 DB 30 RPVHDAREGFLDTLVVH 48  
 |||

RESULT 14  
 ID 092IC2 PRELIMINARY; PRT; 113 AA.  
 AC 092IC2;  
 DT 01-MAY-1999 (TREMblrel. 10, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
 GN p16(INK4a).  
 OS Mus spretus (Western wild mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10096;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRET/El;  
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
 RA Pellicer A., Fernandez-Piqueras J.;  
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
 in mouse inbred strains."  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U79634; AAD00236.1; -  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 2.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1  
 SQ SEQUENCE 113 AA; 12073 MW; C3BFE8325DB2D79E CRC64;

Query Match 12.8%; Score 19; DB 11; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 RPVHDAREGFLDTLVVH 90  
 DB 30 RPVHDAREGFLDTLVVH 48  
 |||

RESULT 15  
 ID 09R0Z3 PRELIMINARY; PRT; 159 AA.  
 AC 09R0Z3;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE p16 PROTEIN p16INK4a.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=F344/N; TRISUE=LUNG;  
 RX MEDLINE=97184461; PubMed=9032263;  
 RA Swaford D.S., Middleton S.K., Palmisano W.A., Nikula K.J.,  
 RA Testaigzi J., Baylin S.B., Herman J.G., Belinsky S.A.;  
 RT "Frequent aberrant methylation of p16INK4a in primary rat lung  
 tumors."  
 RL Mol. Cell. Biol. 17:1366-1374(1997).  
 DR EMBL: L81167; AAD48924.1; -  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 4.  
 DR SMART: SM00248; ANK; 1.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Repeat.  
 SQ SEQUENCE 159 AA; 17366 MW; 3C4CA920A1FEAE86 CRC64;

Query Match 12.8%; Score 19; DB 11; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 RPVHDAREGFLDTLVVH 90  
 DB 72 RPVHDAREGFLDTLVVH 90  
 |||

RESULT 16  
 ID 089088 PRELIMINARY; PRT; 168 AA.  
 AC 089088;  
 DT 01-NOV-1998 (TREMblrel. 08, Created)

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DT 01-NOV-1998 (TREMblrel. 08, last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR p16INK4a (p16INK4a TUMOR SUPPRESSOR
DE PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
GN CDKN2A OR E1ALPHA OR p16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CANP; TISSUE=SPLEEN;
RX MEDLINE=98151529; PubMed=9482902;
RA Zhang S., Ramsay E.S., Mock B.A.;
RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
RT p19ARF, is a candidate for the plasmacytoma susceptibility locus,
RT Pctrl.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
RN [2]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-MA/MAJ;
RX MEDLINE=97179476; PubMed=9021155;
RA Herzog C.R., You M.;
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
RT suppressor gene.";
RL Mamm. Genome 8:65-66(1997).
RN [3]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-BALB/CJ AND MUS POSCHIAVINUS;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044335; AAC08962.1; -
DR EMBL; U49279; AAC00051.1; -
DR EMBL; U79626; AAD00224.1; -
DR HSSP; PA2771; 1B17.
DR MGD; MGI:104738; Cdkn2a.
DR Interpro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KM ANK repeat; Cyclin; Kinase; Repeat.
SQ SEQUENCE 168 AA; 17915 MW; 356A973BEAC4D167 CRC64;

Query Match 12.8%; Score 19; DB 11; Length 168;
Last Local Similarity 100.0%; Pred. No. 5,1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPYHDARREGFLDTLVYLH 90
DB 72 RPYHDARREGFLDTLVYLH 90
P97510
P97510 PRELIMINARY; PRT; 168 AA.
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1999 (TREMblrel. 10, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR p16INK4a (p16INK4a TUMOR SUPPRESSOR
DE PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (p16INK4a) (CYCLIN-
DE DEPENDENT KINASE INHIBITOR PROTEIN).
GN CDKN2A OR E1ALPHA OR p16INK4A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-DBA/2N; TISSUE=SPLEEN;
RX MEDLINE=98151529; PubMed=9482902;
RA Zhang S., Ramsay E.S., Mock B.A.;
RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
RT p19ARF, is a candidate for the plasmacytoma susceptibility locus,
RT Pctrl.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
RN [2]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-DBA/2; AND C57BL/6J X DBA;
RA Malumbres M., de Castro I., Santos J., Melendez B., Mangues R.,
RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-DBA/2; AND C57BL/6;
RX MEDLINE=95380169; PubMed=7651726;
RA Quelle D.E., Ashmun R.A., Hannon G.J., Reinberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";
RL Oncogene 11:635-645(1995).
RN [5]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-DBA/2; AND C57BL/6;
RA Gressani K.M., Rollins L.A., Miller M.S.;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-11 FROM N.A.
RC STRAIN-ICR SWISS;
RX MEDLINE=97128829; PubMed=8973369;
RA Soloff E.V., Herzog C.R., You M.;
RT "The 5'-flanking region of the E1 alpha form of the murine p16INK4a
RT (msl) gene.";
RL Gene 180:213-215(1996).
RN [7]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-CAST/EI, C57BL/6J, ARF/J, AND MOLF/EI;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SVJ;
RA Gong Z., Li J., Fu J.;
RT "Cloning and structure analysis of murine p16INK4a.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044336; AAC08963.1; -
DR EMBL; U49280; AAC00052.1; -
DR EMBL; U66087; AAB39600.1; -
DR EMBL; U66086; AAB39600.1; JOINED.
DR EMBL; AF004588; AAB61416.1; -
DR EMBL; U47018; AAC52987.1; -
DR EMBL; U79628; AAD00226.1; -
DR EMBL; U79625; AAD00223.1; -
DR EMBL; U79627; AAD00225.1; -
DR EMBL; AF332190; AAK83159.1; -
DR HSSP; PA2771; 1B17.
DR MGD; MGI:104738; Cdkn2a.
DR Interpro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KM ANK repeat; Cyclin; Kinase; Repeat.
SQ SEQUENCE FROM N.A.

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SQL SEQUENCE 168 AA; 17941 MW; 9A6B0F24F34D5FEC CRC64;

Query Match 12.8%; Score 19; DB 11; Length 168;

Best Local Similarity 100.0%; Pred. No. 5.1e-10; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPVHDAAREGFLDTLVVL 90  
 DB 72 RPVHDAAREGFLDTLVVL 90

RESULT 18

Q9QWH8 PRELIMINARY; PRT; 113 AA.

AC 09QWH8: 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
 GN p16(INK4A).  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J, RF/J, AND CAST/EI;  
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,

RA Pellicer A., Fernandez-Piqueras J.;  
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences

in mouse inbred strains.";  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U79630; AAD00227.1; -  
 DR HSSP: P42771; 1B17.

DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 2.

DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 DR ANK repeat; Kinase; Repeat.

KW NON\_TER 1  
 FT NON\_TER 1

SQL SEQUENCE 113 AA; 12048 MW; C3A8CF025B94F79E CRC64;

Query Match 12.2%; Score 18; DB 11; Length 113;

Best Local Similarity 100.0%; Pred. No. 3.2e-09; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPVHDAAREGFLDTLVVL 89  
 DB 30 RPVHDAAREGFLDTLVVL 47

RESULT 19

Q9QWH7 PRELIMINARY; PRT; 113 AA.

AC 09QWH7: 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
 GN p16(INK4A).  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=BALB/CJ;

RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
 RA Pellicer A., Fernandez-Piqueras J.;

RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
 in mouse inbred strains.";

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U79631; AAD00228.1; -  
 DR HSSP: P42771; 1B17.

DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 2.

DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.

FT NON\_TER 1  
 FT NON\_TER 1

SQL SEQUENCE 113 AA; 12062 MW; DA99452AF91EC60D CRC64;

Query Match 12.2%; Score 18; DB 11; Length 113;

Best Local Similarity 100.0%; Pred. No. 3.2e-09; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPVHDAAREGFLDTLVVL 89  
 DB 30 RPVHDAAREGFLDTLVVL 47

RESULT 20

Q9QWH6 PRELIMINARY; PRT; 113 AA.

AC 09QWH6: 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
 GN p16(INK4A).  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-MOLF/EI;

RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
 RA Pellicer A., Fernandez-Piqueras J.;

RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
 in mouse inbred strains.";

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U79632; AAD00229.1; -  
 DR HSSP: P42771; 1B17.

DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 2.

DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.

FT NON\_TER 1  
 FT NON\_TER 1

SQL SEQUENCE 113 AA; 12147 MW; C3A8CF025FD4B39E CRC64;

Query Match 12.2%; Score 18; DB 11; Length 113;

Best Local Similarity 100.0%; Pred. No. 3.2e-09; Mismatches 0; Indels 0; Gaps 0;

QY 72 RPVHDAAREGFLDTLVVL 89  
 DB 30 RPVHDAAREGFLDTLVVL 47

RESULT 21

Q97886 PRELIMINARY; PRT; 58 AA.

AC 097886: 01-MAY-1999 (TREMblrel. 10, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE 2A INHIBITOR (FRAGMENT).  
 GN CDKN2A.

OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SKIN;  
 RA Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.,  
 RT "An equine sequence homologous to cyclin-dependent kinase inhibitor  
 (CDKN2A).";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF076782; AAC97110.1;  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 1.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1 58  
 FT SEQUENCE 58 AA; 6162 MW; DP9D90C873C1E6D7 CRC64;

Query Match 10.1%; Score 15; DB 6; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 TLTPRVHDAAREGFL 83  
 |||||  
 DB 44 TLTPRVHDAAREGFL 58

RESULT 22  
 O90WH5 PRELIMINARY; PRT; 113 AA.  
 ID O90WH5;  
 AC O90WH5;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).  
 GN p16(INK4a).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MUS MUSCULUS;  
 RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
 RT Pellicer A., Fernandez-Piqueras J.;  
 RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
 in mouse inbred strains";  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U79633; AAD00230.1;  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR Pfam: PF00023; ank; 2.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Kinase; Repeat.  
 FT NON\_TER 1 113  
 FT SEQUENCE 113 AA; 12170 MW; 5D4DEB325D06638B CRC64;

Query Match 10.1%; Score 15; DB 11; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 RPYHDAAREGFLDTL 86  
 |||||  
 DB 30 RPYHDAAREGFLDTL 44

RESULT 23  
 O9UD00 PRELIMINARY; PRT; 21 AA.

AC O9UD00;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)  
 DE CDKN2 PROTEIN (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95400305; PubMed=7670475;  
 RA Gruis N.A., van der Velde P.A., Sandkuil L.A., Prins D.E.,  
 RT Weaver-Feldhaus J., Kamb A., Bergman W., Frans R.R.;  
 RT "Homologues for CDKN2 (p16) germline mutation in Dutch familial  
 melanoma kindreds";  
 RL Nat. Genet. 10:351-353(1995).  
 SO SEQUENCE 21 AA; 2192 MW; 9424A5E1D7DEAFPS CRC64;

Query Match 9.5%; Score 14; DB 4; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 LLLHGAEPNCADP 67  
 |||||  
 DB 1 LLLHGAEPNCADP 14

RESULT 24  
 O99PH0 PRELIMINARY; PRT; 144 AA.  
 ID O99PH0;  
 AC O99PH0;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE CYCLIN-DEPENDENT CELL CYCLE INHIBITOR (FRAGMENT).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Muscarella P., Knobloch T.J., Weghorst C.M.;  
 RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and  
 RT Identification of Inactivating Alterations in Hamster Tumor Cell  
 Lines";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF291998; AAC59801.1;  
 DR EMBL: AF291997; AAC59801.1; JOINED.  
 DR HSSP: P42771; 1B17.  
 DR InterPro: IPR002110; ANK.  
 DR SMART: SM00248; ANK; 4.  
 DR PROSITE: PS50297; ANK\_REP\_REGION; 1.  
 KW ANK repeat; Repeat.  
 FT NON\_TER 144 144  
 FT SEQUENCE 144 AA; 15206 MW; 8904F9C0C316A084 CRC64;

Query Match 8.1%; Score 12; DB 11; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 0.0019;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 RPYHDAAREGFL 83  
 |||||  
 DB 72 RPYHDAAREGFL 83

RESULT 25  
 O9E033 PRELIMINARY; PRT; 157 AA.  
 ID O9E033;  
 AC O9E033;

DT 01-MAR-2001 (TREMblrel. 16, Created)  
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR 2.  
OC Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OC NCBI\_TaxID=10036;  
OX [1]  
RP SEQUENCE FROM N.A.  
RA Muscarella P., Knobloch T.J., Weghorst C.M.:  
RT "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and  
RT Identification of Inactivating Alterations in Hamster Tumor Cell  
RT Lines."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF292567; AAG44950.1; -.  
DR HSSP; PA2771; 1bit.  
DR InterPro; IPR002110; ANK.  
DR SMART; SM00248; ANK; 4.  
DT PROSITE; PS50297; ANK\_REPEAT; 1.  
KW ANK repeat; Kinase; Repeat.  
SQ SEQUENCE 157 AA; 16635 MW; 06FD66AEB30DCF8 CRC64;

Query Match 8.1%; Score 12; DB 11; Length 157;  
Best Local Similarity 100.0%; Pred. No. 0.002;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 RPYHDAREGFL 83  
DB 72 RPYHDAREGFL 83

RESULT 26

090UJ3 PRELIMINARY; PRT; 44 AA.  
AC 090UJ3;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).  
GN INK4B.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

RA STRAIN-VARIOUS STRAINS;  
RA Santos J., Melendez B., Perez de Castro I., Martin-Rivera L.,  
RA Malumbres M., Serrano M., Pellicer A., Fernandez-Piqueras J.;  
RT "Comparative analysis of the p16 (INK4a) and p15 (INK4b) DNA sequences  
RT in mouse inbred strains."  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U80415; AAD00358.1; -.  
DR EMBL; U80413; AAD00356.1; -.  
DR EMBL; U80414; AAD00357.1; -.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 1.  
DR SMART; SM00248; ANK; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT; 1.  
DR ANK repeat; Cyclin; Kinase; Repeat.  
KW NON\_TER 44  
FT NON\_TER 44  
SQ SEQUENCE 44 AA; 4537 MW; AFBFB6B347AB8B34 CRC64;

Query Match 5.4%; Score 8; DB 11; Length 44;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LATAAARG 15

DB 10 LATAAARG 17

RESULT 27

092IC0 PRELIMINARY; PRT; 44 AA.  
ID 092IC0;  
AC 092IC0;  
DT 01-MAY-1999 (TREMblrel. 10, Created)  
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).  
GN INK4B.

OS Mus spretus (Western wild mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10096;  
RN [1]  
RP SEQUENCE FROM N.A.

RA STRAIN-SPRET/EL;  
RA Santos J., Melendez B., Perez de Castro I., Martin-Rivera L.,  
RA Malumbres M., Serrano M., Pellicer A., Fernandez-Piqueras J.;  
RT "Comparative analysis of the p16 (INK4a) and p15 (INK4b) DNA sequences  
RT in mouse inbred strains."  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
RL EMBL; U80416; AAD00359.1; -.  
DR InterPro; IPR002110; ANK.  
DR Pfam; PF00023; ank; 1.  
DR SMART; SM00248; ANK; 1.

DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT; 1.  
KW ANK repeat; Kinase; Repeat.  
FT NON\_TER 44  
SQ SEQUENCE 44 AA; 4537 MW; AFBFB6B347AB8B34 CRC64;

Query Match 5.4%; Score 8; DB 11; Length 44;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LATAAARG 15  
DB 10 LATAAARG 17

RESULT 28

09WLJ9 PRELIMINARY; PRT; 91 AA.  
ID 09WLJ9;  
AC 09WLJ9;  
DT 01-NOV-1999 (TREMblrel. 12, Created)  
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
DE NONSTRUCTURAL POLYPROTEIN (FRAGMENT).  
OS Hepatitis E virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage.  
OX NCBI\_TaxID=12461;  
RN [1]  
RP SEQUENCE FROM N.A.

RA MEDLINE=99013657; PubMed=9797311.  
RA STRAIN=BCN;  
RA Pina S., Jofre J., Emerson S.U., Purcell R.H., Girones R.;  
RT "Characterization of a strain of infectious hepatitis E virus isolated  
RT from sewage in an area where hepatitis E is not endemic."  
RL Appl. Environ. Microbiol. 64:4485-4488(1998).  
DR EMBL; AF061581; AAC77806.1; -.  
KW Polyprotein.

FT NON\_TER 1  
FT NON\_TER 91  
SQ SEQUENCE 91 AA; 10056 MW; 9017B9EC0CBA3A43 CRC64;

Query Match 5.4%; Score 8; DB 12; Length 91;  
Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 LAELGHR 116  
|||||||

Db 7 LAELGHR 14

RESULT 29

Q9M618 PRELIMINARY; PRT; 124 AA.

AC Q9M618:

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DR P13CDKN2X.

GN CDKN2X.

OS Xiphophorus helleri.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Cyprinodontiformes; Poeciliidae; Xiphophorus.

NCBI\_TaxID=8084;

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RT Xiphophorus Fish Melanoma Model."

RL EMBL: AF132500; MAD21313.1; -.

DR HSSP: P42771; 1B17.

DR InterPro: IPR002110; ANK.

DR Pfam: PF00023; ank; 3.

DR SMART: SM00248; ANK; 1.

DR PROSITE: PS50088; ANK\_REPEAT; 1.

DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.

KW ANK repeat; Repeat.

SQ SEQUENCE 124 AA; 13049 MW; 47F354B1BD27BD3F CRC64;

Query Match 5.4%; Score 8; DB 13; Length 124;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IOVMMGMS 48  
|||||||

Db 40 IOVMMGMS 47

RESULT 30

P70067 PRELIMINARY; PRT; 124 AA.

AC P70067:

DT 01-FEB-1997 (TREMBLrel. 02, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE 13CDKN2X PROTEIN.

GN CDKN2X.

OS Xiphophorus maculatus (Southern platyfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Cyprinodontiformes; Poeciliidae; Xiphophorus.

NCBI\_TaxID=8083;

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RT Xiphophorus Fish Melanoma Model."

RL EMBL: U69273; AAB09560.3; -.

DR HSSP: P42771; 1B17.

DR InterPro: IPR002110; ANK.

DR Pfam: PF00023; ank; 3.

DR SMART: SM00248; ANK; 1.

DR PROSITE: PS50088; ANK\_REPEAT; 2.

DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.

KW ANK repeat; Repeat.

SQ SEQUENCE 124 AA; 13034 MW; 47F3C093707BD25 CRC64;

Query Match 5.4%; Score 8; DB 13; Length 124;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IOVMMGMS 48  
|||||||

Db 40 IOVMMGMS 47

RESULT 31

P89468 PRELIMINARY; PRT; 300 AA.

AC P89468:

DT 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE TEGUMENT PROTEIN.

GN UL49.

OS Herpes simplex virus (type 2).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.

NCBI\_TaxID=10310;

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RT Herpes simplex virus type 2 genome: unique component of the herpes simplex virus type 2 genome: identification of the gene encoding glycoprotein G, and evolutionary comparisons."

RL J. Gen. Virol. 68:19-38(1987).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN-HG52;

RC MEDLINE=90278430; PubMed=2161906;

RA Everett R., Fenwick M.;

RT "Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52 encodes a truncated UL41 product."

RL J. Gen. Virol. 71:1387-1390(1990).

[3]

RP SEQUENCE FROM N.A.

RC STRAIN-HG52;

RC MEDLINE=92113549; PubMed=1662697;

RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;

RT "Comparative sequence analysis of the long repeat regions and adjoining parts of the long unique regions in the genomes of herpes simplex viruses types 1 and 2."

RL J. Gen. Virol. 72:3057-3075(1991).

[4]

RP SEQUENCE FROM N.A.

RC STRAIN-HG52;

RL Proc. Natl. Acad. Sci. U.S.A. 93:13042-13047(1996).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN-JP 163 A; TISSUE=MUSCLE;

RA Kazianis S., Morizot D.C., Della Coletta L., Johnston D.A., Woolcock B., Vielkind J.R., Nairn R.S.;

RT "Comparative Structure and Characterization of a CDKN2 Gene in a Xiphophorus Fish Melanoma Model."

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: U69273; AAB09560.3; -.

DR HSSP: P42771; 1B17.

DR InterPro: IPR002110; ANK.

DR Pfam: PF00023; ank; 3.

DR SMART: SM00248; ANK; 1.

DR PROSITE: PS50088; ANK\_REPEAT; 2.

DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.

KW ANK repeat; Repeat.

SQ SEQUENCE 124 AA; 13034 MW; 47F3C093707BD25 CRC64;

Query Match 5.4%; Score 8; DB 13; Length 124;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 IOVMMGMS 48  
|||||||

Db 40 IOVMMGMS 47

RESULT 31

P89468 PRELIMINARY; PRT; 300 AA.

AC P89468:

DT 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE TEGUMENT PROTEIN.

GN UL49.

OS Herpes simplex virus (type 2).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.

NCBI\_TaxID=10310;

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RT Herpes simplex virus type 2 genome: unique component of the herpes simplex virus type 2 genome: identification of the gene encoding glycoprotein G, and evolutionary comparisons."

RL J. Gen. Virol. 68:19-38(1987).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN-HG52;

RC MEDLINE=90278430; PubMed=2161906;

RA Everett R., Fenwick M.;

RT "Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52 encodes a truncated UL41 product."

RL J. Gen. Virol. 71:1387-1390(1990).

[3]

RP SEQUENCE FROM N.A.

RC STRAIN-HG52;

RC MEDLINE=92113549; PubMed=1662697;

RA McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;

RT "Comparative sequence analysis of the long repeat regions and adjoining parts of the long unique regions in the genomes of herpes simplex viruses types 1 and 2."

RL J. Gen. Virol. 72:3057-3075(1991).

[4]

RP SEQUENCE FROM N.A.

RC STRAIN-HG52;